



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 167604

TO: Catherine Joyce
Location: REM/4C04/3C18
Art Unit: 1642
Tuesday, October 04, 2005

Case Serial Number: 10/645094

From: Edward Hart
Location: Biotech-Chem Library
REM-1A55
Phone: 571-272-2512

edward.hart@uspto.gov

Search Notes

Examiner Joyce,

Here are the results of the search you requested.

Please feel free to contact me if you have any questions.

Edward Hart

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STIC-Biotech/ChemLib

167604

From: Joyce, Catherine
Sent: Monday, October 03, 2005 4:11 PM
To: STIC-Biotech/ChemLib
Subject: 10/645094

Please search the following sequences:

SEQ ID NO:1 (polypeptide)

Catherine Joyce
Art Unit 1642
Ph. 571-272-3321
Office: 4C04
Mailbox: 3C18

RECEIVED
OCT -4 2005
STIC/BIOTECH/CHM LIB
(STIC)

Searcher: _____
Searcher Phone: _____
Date Searcher Picked up: 10/4/05
Date completed: 10/4/05
Searcher Prep Time: _____
Online Time: _____

Type of Search 1
NA# _____ AA# _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure #: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable
STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: DP
WWW/Internet: _____
Other (Specify): _____

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Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension **.rup**) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:

<http://www.pir.uniprot.org/database/archive.shtml>

If you have any questions regarding this information or your results, please contact any STIC searcher.

When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.

✓

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Pending Nucleic Acid and Pending Amino Acid database searches generate two sets of results each. The Pending databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Searches run against the Nucleic Acid Pending database produce two sets of results, with the extensions .rnpm and .rnpn

Searches run against the Amino Acid Pending database produce two sets of results, with the extensions .rapm and .rapn

Because they contain data that is confidential, the results of Pending database searches should not be left in the case .

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STIC SEARCH RESULTS FEEDBACK FORM

Biotech-Chem Library

Questions about the scope or the results of the search? Contact *the searcher* or contact:

Mary Hale, Information Branch Supervisor
Remsen Bldg. 01 D86
571-272-2507

Voluntary Results Feedback Form

➤ I am an examiner in Workgroup: Example: 1610

➤ Relevant prior art **found**, search results used as follows:

- ☐ 102 rejection
- ☐ 103 rejection
- ☐ Cited as being of interest.
- ☐ Helped examiner better understand the invention.
- ☐ Helped examiner better understand the state of the art in their technology.

Types of relevant prior art found:

- ☐ Foreign Patent(s)
- ☐ Non-Patent Literature
(journal articles, conference proceedings, new product announcements etc.)

➤ Relevant prior art **not found**:

- ☐ Results verified the lack of relevant prior art (helped determine patentability).
- ☐ Results were not useful in determining patentability or understanding the invention.

Comments:

Drop off or send completed forms to STIC-Biotech-Chem Library Remsen Bldg.



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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 4, 2005, 13:46:40 ; Search time 180 Seconds
(without alignments)
1490.719 Million cell updates/sec

Title: US-10-645-094-1
Perfect score: 2703
Sequence: 1 MNLHVWKLSVSVLITLY.....TNINKVANEESTIETKDEL 524

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues
Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2699	99.9	524	2 Q918A7	Q918A7 scomber jap
2	1156.5	42.8	523	2 Q8VEN4	Q8VEN4 mus musculus
3	1096.5	40.6	504	2 Q90W54	Q90W54 agkistrodon
4	1089.5	40.3	504	2 Q6STF1	Q6STF1 agkistrodon
5	1079.5	39.9	516	1 OXLA AGKRH	P81382 agkistrodon
6	1063.5	39.3	516	2 Q9PWC9	Q9PWC9 croctalus at
7	1059.5	39.2	497	2 Q6TGO9	Q6TGO9 bothrops ja
8	1059.5	39.2	516	1 OXLA CROAD	Q93364 croctalus ad
9	1058.5	39.2	478	2 Q6TGO8	Q6TGO8 bothrops mo
10	1055.5	39.0	516	2 Q6WP39	Q6WP39 trimeresuru
11	1052.5	38.9	516	2 Q7T062	Q7T062 trimeresuru
12	1048.5	38.8	523	2 Q9JJK6	Q9JJK6 mus musculus
13	1034	38.3	630	1 FIG1 MOUSE	O09046 mus musculus
14	1034	38.3	630	2 Q6YBV6	Q6YBV6 mus musculus
15	1034	38.3	630	2 Q6YDI8	Q6YDI8 mus musculus
16	1030	38.1	630	2 Q6Y632	Q6Y632 mus musculus
17	999	37.0	567	1 FIG1 HUMAN	Q96R99 homo sapien
18	999	37.0	588	2 Q8TEM5	Q8TEM5 homo sapien
19	999	37.0	588	2 Q6P2Q3	Q6P2Q3 homo sapien
20	823.5	30.5	490	2 Q739P2	Q739P2 bacillus ce
21	818.5	30.3	482	2 Q81EG3	Q81EG3 bacillus ce
22	818.5	30.3	485	2 Q31334	Q31334 bacillus ce
23	817.5	30.2	478	2 Q81RW3	Q81RW3 bacillus th
24	812.5	30.1	485	2 Q6HJU8	Q6HJU8 bacillus th
25	807.5	29.9	482	2 Q63CE2	Q63CE2 bacillus an
26	807.5	29.9	482	2 Q81RM4	Q81RM4 bacillus an
27	796.5	29.5	478	2 Q739X9	Q739X9 bacillus ce
28	777.5	28.8	478	2 Q63CN0	Q63CN0 bacillus ce
29	773.5	28.6	478	2 Q6HK30	Q6HK30 bacillus th
30	761.5	28.2	478	2 Q81EP3	Q81EP3 bacillus ce
31	751	27.8	509	2 Q8R2G8	Q8R2G8 mus musculus

RESULT 1

Q918A7

ID Q918A7 PRELIMINARY; PRT; 524 AA.

AC Q918A7; 27.3 446 2 O34363

DT 01-OCT-2000 (Tremblrel. 15, Created)

DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)

DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)

DE Endoplasmic reticulum lumenal L-amino acid oxidase precursor.

GN Name=lao;

OS Scomber japonicus (Chub mackerel).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;

OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Scombroidei;

OC Scombridae; Scomber.

OX NCBI_TaxID=13676;

RN [1]_TaxID=13676;

RP SEQUENCE FROM N.A.

RX MEDLINE=20363938; PubMed=10903755;

RA Jung S.K., Mai A., Iwamoto M., Arizono N., Fujimoto D., Sakamaki K.,

RA Yonehara S.;

RT "Purification and cloning of an apoptosis-inducing protein derived

RT from fish infected with Anisakis simplex, a causative nematode of

RT human anisakiasis.;"

RL J. Immunol. 165:1491-1497(2000).

DR EMBL; AJ400871; CAC00499.1; -.

DR HSSP; P81382; 1F8S.

DR GO; GO:0016491; P:oxidoreductase activity; IEA.

DR GO; GO:0006118; P:electron transport; IEA.

DR InterPro; IPR000759; Adrnxd_reductase.

DR InterPro; IPR001613; Amino oxidase.

DR InterPro; IPR002937; Amino oxidase.

DR InterPro; IPR000886; ER target_S.

DR InterPro; IPR000205; NAD BS.

DR Pfam; PF01593; Amino oxidase; 1.

DR PRINTS; PR00419; ADXRD7ASE.

DR PRINTS; PR00757; AMINEOXDASEF.

DR PROSITE; PS00014; ER_TARGET; UNKNOWN_1.

KW Signal.

FT SIGNAL. 1 30 Potential.

FT CHAIN. 31 524 endoplasmic reticulum lumenal L-amino acid oxidase.

FT SEQUENCE 524 AA; 58623 MW; 5C17ACA07E74897E CRC64;

Query Match 99.9%; Score 2699; DB 2; Length 524;

Best Local Similarity 99.8%; Pred. No. 1.6e-158;

Matches 523; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNLHVWKLSVSVLITLYSHTVALSLKEHLADCLDKDYDTLLQTLNGLPHINTSH 60

Db 1 MNLHVWKLSVSVLITLYSHTVALSLKEHLADCLDKDYDTLLQTLNGLPHINTSH 60

QY 61 HWIVGAGMAGLTAALKLQDAGHTVTILEANDRVGRVETVNEKEGYAENGAMRIPSS 120

Db 61 HWIVGAGMAGLTAALKLQDAGHTVTILEANDRVGRVETVNEKEGYAENGAMRIPSS 120

DR	HSSP; P81382; 1P8R.
DR	MGD; MGI:2140628; Laol.
DR	GO; GO:0005615; C:extracellular space; TAS.
DR	GO; GO:0001716; F:L-amino acid oxidase activity; IDA.
DR	GO; GO:0009063; P:amino acid catabolism; IDA.
DR	Pfam; PF01593; Amino oxidase; 1.
DR	PRINTS; PR00419; ADXEDTASE.
DR	PRINTS; PR00757; AMINEOXIDASEF.
DR	PRINTS; PR00370; PMOXYGENASE.
SQ	SEQUENCE 523 AA; 58028 MW; F6D31592D7117A0B CRC64;
Query Match	42.8%; Score 1156.5; DB 2; Length 523;
Best Local Similarity	47.1%; Pred. No. 3.6e-63;
Matches 235; Conservative 85; Mismatches 172; Indels 7; Gaps 4;	
QY	27 LSLKEHLADCLDEKDYDTLLQTLDNGLPHINTSHHVIVVAGMAGLTAALKLLQDAGHTVT 86
Db	25 LALYENLVKCFQDPDEAFLLIAQNLHTSPLSKRVVVVAGMAGLVAAKTLQDAGHEVT 84
QY	87 ILEANDRVGGRVETRYRNEKEGYAEMGAMRIPSSHRIVQWFKVLGVEMNEFVMTDDNTF 146
Db	85 ILEASNHIGGRVVTLRNKEEGWYLELGPMPRI PESHKLIHTYVQKLGKLNKFNQYDSNTW 144
QY	147 YLVNGVRETYVVOENPDVLYKYNVSESEKIGISADLLDRALQKVEEVEANGCKAALEKY 206
Db	145 YLLNGQRYRASEVMANPGILGYPLRPSEKNTVTDLFYQAITKIKPHRKTSNCSQLLSLY 204
QY	207 DRYSVKEYLKEEGGLSPGAVRMIGDGLNEOSLMYTALSEMIYDQADVNDVSYTHEVTGGS 266
Db	205 DSYSTKAYLMKEGTLKGAIEIMGIDIMNENAGYKSLLESIRLASIFSKSDQSEITGGF 264
QY	267 DLLPEAF-LSVLDVPILLNSKVKHIRQSDKGVIVSYQT-GNESSLMPLDLSADIVLVTTAK 324
Db	265 DQPLNGLSASLKPCTIRLGSKVERVVRDGPVKVMYRTDGTPTSAHLKLTADYAIITASAK 324
QY	325 AALFIDPDPPLSISKMEALRSVHSDSTKILLTPRDKFWEDDGIKGGKSIDGSPSRIYY 384
Db	325 ATRLITFPPLSREKTHALRSVHTSATKVVLCNERFWEQDGIKGGYSITDRPSRFIY 384
QY	385 PSHSFHTNETIGVLLASVTWSDSLLFLGASDEELKELALRDLAKIH---GEQVMDKCTG 441
Db	385 PSHSLPGGK--GVLLASFTVGDDSSFFAALKPNQVVDVLDLAAVHRIPKEELKRCMKPK 442
QY	442 VIVKWSADPYSIGAFALFTPYOHLBYAQELFSSEGRVHFAGETAPPHAWIETSMKSAI 501
Db	443 SAIKHSWLDPLTIGATFEFTPYQFVDYSKQLSQPEGRIFYFAGEHTCLPHSWIDTAIKSGI 502
QY	502 RAATNINKVANEESTIHT 520
Db	503 RASCNIAQAVDKAETRGT 521
QY	Q90W54 PRELIMINARY; PRT; 504 AA.
AC	Q90W54;
DT	01-DEC-2001 (T-EMBLrel. 19, Created)
DT	01-DEC-2001 (T-EMBLrel. 19, Last sequence update)
DT	01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE	M-LAO precursor (EC 1.4.3.2).
OS	Agkistrodon halsys blomhoffii (Mamushi) (Gloydus blomhoffii).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC	Viperidae; Crotalinae; Gloydus.
OX	NCBI_TaxID=242054;
RP	[1]
RP	SEQUENCE FROM N.A.
RC	TISSUE=Venom;
RX	MEDLINE=21240157; PubMed=11341935; DOI=10.1016/S0167-4838(00)00229-6;
RA	Takatsuka H., Sakurai Y., Yoshioka A., Kokubo T., Usami Y., Suzuki M.,
RA	Matsui T., Titani K., Yagi H., Matsumoto M., Fujimura Y.;
RT	"Molecular characterization of L-amino acid oxidase from Agkistrodon
RT	halsys blomhoffii with special reference to platelet aggregation.";


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RT rhodostoma:comparative sequence analysis and characterization of
RT active and inactive forms of the enzyme.";
RL Eur. J. Biochem. 268:1679-1686(2001).
RN [2]
RP SEQUENCE OF 19-38 FROM N.A.
RX TISSUE=Venom;
RX MEDLINE=94361525; PubMed=8080286; DOI=10.1006/abbi.1994.1401;
RA Ponudurai G., Chung M.C.M., Tan N.-H.;
RT "Purification and properties of the L-amino acid oxidase from Malayan
RT pit viper (Calloselasma rhodostoma) venom.";
RL Arch. Biochem. Biophys. 313:373-378 (1994).
RN [3]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS), AND CARBOHYDRATE-LINKAGE SITES.
RX TISSUE=Venom;
RX MEDLINE=20402326; PubMed=10944103; DOI=10.1093/emboj/19.16.4204;
RA Pawelek P.D., Cheah J., Coulombe R., Macheroux P., Ghisla S.,
RA Vrieland A.;
RT "The structure of L-amino acid oxidase reveals the substrate
RT trajectory into an enantiomerically conserved active site.";
RL EMBO J. 19:4204-4215(2000).
CC -!- FUNCTION: Catalyzes an oxidative deamination of predominantly
CC hydrophobic and aromatic L-amino acids. Has an antibacterial
CC effect and an ability to induce apoptosis. The H(2)O(2) produced
CC by L-amino acid oxidation is involved in the apoxin-I induced
CC apoptosis and hemorrhage caused by the venom.
CC -!- CATALYTIC ACTIVITY: An L-amino acid + H(2)O + O(2) = a 2-oxo acid
CC + NH(3) + H(2)O(2).
CC -!- COFACTOR: FAD.
CC -!- SUBUNIT: Homodimer.
CC -!- MISCELLANEOUS: Has a pH optimum of 9.0, a determined pI of 4.4 and
CC is temperature stable.
CC -!- SIMILARITY: Belongs to the flavin monooxygenase family.
CC Strong, to mammalian FIC1.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AJ271725; CAB71136.1; -.
DR PDB; 1F88; X-ray; A/B/C/D=19-516.
DR PDB; 1F88; X-ray; A/B/C/D/E/F/G/H=19-516.
DR GlycoSuiteDB; P81382; -.
DR InterPro; IPR000759; Adrndx_reductase.
DR InterPro; IPR001613; Amineoxidfl.
DR InterPro; IPR002937; Amino_oxidase.
DR InterPro; IPR000205; NAD_BS.
DR Pfam; PF01593; Amino_oxidase; 1.
DR PRINTS; PR00419; ADXRDTASE.
DR PRINTS; PR00757; AMINEOXDASEF.
KW 3D-structure; Direct protein sequencing; FAD; Flavoprotein;
KW Glycoprotein; Oxidoreductase; Signal; Toxin.
FT SIGNAL 1 18
FT CHAIN 19 516 L-amino-acid oxidase.
FT NP_BIND 52 108 FAD (ADP part) (Potential).
FT CARBOHYD 190 190 N-linked (GlcNAc...).
FT CARBOHYD 379 379 N-linked (GlcNAc...).
FT CONFLICT 28 28 C -> E (in Ref. 2).
FT CONFLICT 33 33 D -> N (in Ref. 2).
FT TURN 24 25
FT HELIX 26 29
FT TURN 32 33
FT HELIX 34 43
FT STRAND 53 57
FT STRAND 60 60
FT HELIX 61 72
FT TURN 73 74
FT TURN 76 80
FT STRAND 87 87
FT TURN 88 89
SQ SEQUENCE 516 AA; 58221 MW; 5F9435718B3A3BDE CRC64;
39.9%; Score 1079.5; DB 1; Length 516;
Query Match

```

		Best Local Similarity 44.4%; Pred. No. 2e-58; Matches 219; Conservative 92; Mismatches 175; Indels 7; Gaps 5;	
QY	33	LADCLDQDYDTLLQTLONGLPHINTSHHVVIVGAGMAGLTAAKLLQDAGHTVTTILEAND 92	
DB	25	LAECFQDYEFELETARNGLKATSNPKKVVIVGAGMAGLSAAVLAGAGHQVTVLEASE 84	
QY	93	RVGGRVETYNKEGWAEMGAMRIPSSHRIQVQFVKKLGVMNEFVMTDDNTFYLVNGV 152	
DB	85	RPGGRVTRNBEAGWYANLGPMLPEKHRIVREYIRKFDLRLNEFSQENDNANWYFIKI 144	
QY	153	RRTYVQVQNPVULKNNVSESEKGSADLLDRALOKVKEVEANGCKAALKYDRYSVK 212	
DB	145	RKVGVEKDPGLLKYPVPSEAGSAGQLYEESLGKVVVEELKRTNCSYILNKYDTYSTK 204	
QY	213	EYLKEGGSLPGAVRMIGDGLLNEQSLMYTALSEMIYDQADVNDVSYHYHEVTGSDLLPEA 272	
DB	205	EYLKEGGSLPGAVRMIGDGLLNEQSLMYTALSEMIYDQADVNDVSYHYHEVTGSDLLPEA 264	
QY	273	FLSLVDVPIILLNSKVKHIRQSKGVIVSYQTGNESLMDLSADIIVLVTTTAKAALFIDPD 332	
DB	265	MYRDIQDKVHFNAQVLIKIQNDQKVTYVYELSKET-PSVTADYIVICTTSRAVRLIKFN 323	
QY	333	PPLSISKMBALRSVHYDSSTKILLTRDKFWEDDGIKRGKSTIDGFSRVIYYPSPSHFN 392	
DB	324	PPLPKKAHALRSVHYRSCTKIFLTCTTKFWEDDGIHGGKSTTDLPSRFIYYPNHNF-TN 382	
QY	393	ETIGVLLASYTWSDESLLFLGASDEELKELALDLAKIH--GEQWMDKCTGVIVVK 449	
DB	383	-GVGVIIA-YGIGDDANFFQALDFKDCADIVINDLSLIHQPKDIOQSCYPSVTKQWSL 440	
QY	450	DPSYSLGAFALFTPYQHLEVAQELFSSEGRVHFAGEHTAPPHAWIETSMKSAIRAATNINK 509	
DB	441	DKYANGGITTTFTPYQFHFSEALTAQRIYFAGEYTAQAHGWIDSTIKSGLRARDVNL 500	
QY	510	VANEESTIEHTKD 522	
DB	501	ASENPSPGIHLSND 513	
RESULT 6		PRELIMINARY; PRT; 516 AA.	
ID	Q9PWC9		
AC	Q9PWC9		
DT	01-MAY-2000 (TrEMBLrel. 13, Created)		
DT	01-MAY-2000 (TrEMBLrel. 13, Last sequence update)		
DT	01-OCT-2003 (TrEMBLrel. 25, Last annotation update)		
DE	FAD-containing L-amino acid oxidase Apoxin 1.		
OS	Crotalus atrox (Western diamondback rattlesnake).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;		
OC	Viperidae; Crotalinae; Crotalus.		
OX	NCBI_TaxID=8730;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Venom gland;		
RA	Torii S., Mashima T., Naito M., Haga N., Yamane K., Yamamoto K.,		
RA	Fox J.W., Tsuruo T.;		
RL	Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AF093248; AAD45200.1; -.		
DR	HSSP; P81382; 1F8R.		
DR	GO; GO:0016491; F:oxidoreductase activity; IEA.		
DR	GO; GO:0006118; P:electron transport; IEA.		
DR	InterPro; IPR000759; Adrxn_reductase.		
DR	InterPro; IPR002937; Amino_oxidase.		
DR	InterPro; IPR000205; NAD_BS.		
DR	InterPro; IPR00103; Pyridine_redox_2.		
DR	Pfam; PF01593; Amino_oxidase; 1.		
DR	PRINTS; PR00419; ADXRDTASE.		
DR	PRINTS; PR00469; PNDRDTASEII.		
SQ	SEQUENCE 516 AA; 58766 MW; 6CB90A49A0C015E5 CRC64;		
Query Match		39.3%;	Score 1063.5; DB 2; Length 516;
Best Local Similarity		45.1%;	Pred. No. 3.3e-57;

		Best Local Similarity 44.0%; Pred. No. 2e-57; Matches 218; Conservative 96; Mismatches 169; Indels 13; Gaps 7;	
QY	33	LADCLDQDYDTLLQTLONGLPHINTSHHVVIVGAGMAGLTAAKLLQDAGHTVTTILEAND 92	
DB	25	LEECFRETDEBEFLKAKNGLTATSNPKRVIVGAGMAGLSAAVLAGAGHQVTVLEASE 84	
QY	93	RVGGRVETYNKEGWAEMGAMRIPSSHRIQVQFVKKLGVMNEFVMTDDNTFYLVNGV 152	
DB	85	RVGGRVTRNBEAGWYANLGPMLPEKHRIVREYIRKFDLRLNEFSQENDNANWYFIKI 142	
QY	153	RRTYVQVQNPVULKNNVSESEKGSADLLDRALOKVKEVEANGCKAALKYDRYSVK 212	
DB	143	RKRREVKNPGLLEYPVKPSEEGKSAQLYVESLRKVVVKELKRTNCKYILDKYDTYSTK 202	
QY	213	EYLKEGGSLPGAVRMIGDGLLNEQSLMYTALSEMIYDQADVNDVSYHYHEVTGSDLLPEA 272	
DB	203	EYLKEGGSLPGAVRMIGDGLLNEQSLMYTALSEMIYDQADVNDVSYHYHEVTGSDLLPEA 262	
QY	273	FLSLVDVPIILLNSKVKHIRQSKGVIVSYQTGNESLMDLSADIIVLVTTTAKAALFI 329	
DB	263	MYEAIKEKVQVHFNAQVIEIQNDREATVYQTSANEMS--SVTADYIVICTTSRAARI 320	
QY	330	DFDPLSISKMBALRSVHYDSSTKILLTRDKFWEDDGIKRGKSTIDGFSRVIYYPSPSHF 389	
DB	321	KFEPPLPKKAHALRSVHYRSCTKIFLTCKKKFWEDDGIKRGKSTTDLPSRFIYYPNHN 380	
QY	390	HTNETIGVLLASYTWSDESLLFLGASDEELKELALDLAKIH--GEQWMDKCTGVIVVK 446	
DB	381	TSG--VGVIIA-YGIGDDANFFQALDFKDCADIVINDLSLIHQPKEDIQTFCRPSMIOR 437	
QY	447	WSADPSYSLGAFALFTPYQHLEVAQELFSSEGRVHFAGEHTAPPHAWIETSMKSAIRAATN 506	
DB	438	WLDKYANGGITTTFTPYQFHFSEALTAQRIYFAGEYTAQAHGWIDSTIKSGLTAARD 497	
QY	507	INKVANEESTIEHTKD 522	
DB	498	VNRASENPSPGIHLSND 513	
RESULT 7		PRELIMINARY; PRT; 497 AA.	
ID	Q6TGO9		
AC	Q6TGO9		
DT	05-JUL-2004 (TrEMBLrel. 27, Created)		
DT	05-JUL-2004 (TrEMBLrel. 27, Last sequence update)		
DT	05-JUL-2004 (TrEMBLrel. 27, Last annotation update)		
DE	L-amino acid oxidase (Fragment).		
OS	Bothrops jararacussu (Jararacussu).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;		
OC	Viperidae; Crotalinae; Bothrops.		
OX	NCBI_TaxID=8726;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	Soares A.M., Kashima S., Roberto P.G., Astolfi-Filho S., Pereira J.O.,		
RA	Giglio J.R., Franca S.C.;		
RL	Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AY398691; AAR31182.1; -.		
DR	GO; GO:0004497; P:monooxygenase activity; IEA.		
DR	GO; GO:0006118; P:electron transport; IEA.		
DR	InterPro; IPR000759; Adrxn_reductase.		
DR	InterPro; IPR000960; Flav_cont_mnoxgn.		
DR	InterPro; IPR000205; NAD_BS.		
DR	PRINTS; PR00419; ADXRDTASE.		
DR	PRINTS; PR00757; AMINEOXDASEF.		
DR	PRINTS; PR00370; FMOXYGENASE.		
FT	NON_TER 497		
SQ	SEQUENCE 497 AA; 56288 MW; 51AFCEB28038399A1 CRC64;		
Query Match		39.2%;	Score 1059.5; DB 2; Length 497;
Best Local Similarity		45.1%;	Pred. No. 3.3e-57;

Matches 212; Conservative 85; Mismatches 166; Indels 7; Gaps 4;

QY 33 LADCLEDKDYTLQTLNDLNGLPHTSHHVIVGVAGMAGLTAALKLQDAGHTVILEAND 92
DB 20 LEECFRETDEYEFLEAKNGLSTTSNPKEVIVGVAGMAGLTAALKLQDAGHTVILEAND 79

QY 93 RVGGRVETVRNKEGMYAEMGAMRIPSSHRIVQVFKLGVEMNEFVMTDDNTFYLVNGV 152
DB 80 RAGGQVKTNRNKEGMYANLGMRLPEKHRIVREVIRKFGQLQNEFSGENENAWYFIKNI 139

QY 153 RERTVVOENPDVLKYNVSEKGLSADLLDRLALQKVEEANGCKAALEKYDRYSVK 212
DB 140 RKRGEVNDKPGVLDYVPKPSVSGSAGOLYEEISQKAVEELRRNCTSMYLNKYDTYSTK 199

QY 213 EYLKEEGLSPGAVRMIGDNLNEQSLMTYALSEMIYDQADVNDSTVYHEVTGSGDLLPEA 272
DB 200 EYLLKEGNLSPGAVDMIGDNLNEDSGYVSFIESLKHDDIFAYEKRFEIVGGMDKLTPTS 259

QY 273 FLUSLVDVPIILNSKVKHQRQSKGVIVSYQTGNESSLMDLSADIVLVTTTAKAALFIDFD 332
DB 260 MYQAIQEKVHLNARVIKIQDDVKEVTIVYT-QSEKTLSTVADYIVVCTTSRAARRIKFE 318

QY 333 PPLSISKMEALRSVHYDSSTKILLTFRDKFWEDDGIKRGKSTIDGSPSVIYYPSSHPTN 392
DB 319 PPLPKKAHALRSVHYRSGTKIFLTCTKFWEDDGIHGKSTIDGSPSVIYYPSSHPTN 378

QY 393 ETIGVLLASYTWSDESLLFLGASDBELKELALRLAKIH---GEQVMDKCTGVIVKWSA 449
DB 379 --VGVIIA-YGIGDDANFFQALDPKOCADIVINDLSLHLPKEDIOFTCHPSMIQR 437

QY 450 DYSISGAFALFTPYQHLEYAQELFSSEGRVHFACEHTAFPHAWTSMKSAIRAAATN 506
DB 436 DRYAMGGITTTPTPYQFQHFSEALTAPVDRIYPAGEYTAQAAGHWIASTIKS 485

RESULT 8

OXLA CROAD STANDARD; PRT; 516 AA.

AC O93364;
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE L-amino-acid oxidase precursor (EC 1.4.3.2) (LAO) (LAO) (Apoxin I).
OS Crotalus adamanteus (Eastern diamondback rattlesnake).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidodactylia; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Crotalus.
OX NCBI_TaxID=8729;

RP [1]
RN SEQUENCE FROM N.A., AND SEQUENCE OF 19-44 AND 106-130.
RC TISSUE=Venom;
RX MEDLINE=98369573; PubMed=9703950; DOI=10.1006/bbrc.1998.9024;
RA Raibekas A.A., Massey V.;
RT "Primary structure of the snake venom L-amino acid oxidase shows high
RT homology with the mouse B cell interleukin 4-induced Fcγ protein.";
RL Biochem. Biophys. Res. Commun. 248:476-478 (1998).
CC -!- FUNCTION: Catalyzes an oxidative deamination of predominantly
CC hydrophobic and aromatic L-amino acids. Has an antibacterial
CC effect and an ability to induce apoptosis. The H(2)O(2) produced
CC by L-amino acid oxidation is involved in the apoxin-I induced
CC apoptosis and hemorrhage caused by the venom.
CC -!- CATALYTIC ACTIVITY: An L-amino acid + H(2)O + O(2) = a 2-oxo acid
CC + NH(3) + H(2)O(2).
CC -!- COFACTOR: FAD.
CC -!- SUBUNIT: Homodimer.
CC -!- PTM: Glycosylated.
CC -!- SIMILARITY: Belongs to the flavin monooxygenase oxidase family.
CC Strong, to mammalian FcγI.
CC -!- DATABASE: NAME=Worthington enzyme manual;
CC WWW="http://www.worthington-biochem.com/LAO/".
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
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CC or send an email to license@iesb-sib.ch).
CC -----
DR EMBL; AF071564; AAC32267.1; -.
DR PIR; J02666; J02666.
DR HSSP; P81382; 1F8R.
DR InterPro; IPR000759; Adnrx_reductase.
DR InterPro; IPR002937; Amino_oxidase.
DR InterPro; IPR002050; NAD_BS.
DR InterPro; IPR00103; Pyridine_redox_2.
DR Pfam; PF01593; Amino_oxidase; 1.
DR PRINTS; PR00419; ADXRDTASE.
DR PRINTS; PR00469; PNDRDPTASEII.
KW Antibiotic; Apoptosis; Direct protein sequencing; FAD; Flavoprotein;
KW Glycoprotein; Oxidoreductase; Signal; Toxin.
FT CHAIN 1 18
FT NP_BIND 19 516 L-amino-acid oxidase.
FT CARBOHYD 52 106 FAD (ADP part) (Potential).
FT SEQUENCE 379 379 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 516 AA; 58662 MW; PFAA77A49FDA05A_CRC64;

Query Match 39.2%; Score 1059.5; DB 1; Length 516;
Best Local Similarity 44.0%; Pred. No. 3.5e-57;
Matches 218; Conservative 94; Mismatches 171; Indels 13; Gaps 7;

QY 33 LADCLEDKDYTLQTLNDLNGLPHTSHHVIVGVAGMAGLTAALKLQDAGHTVILEAND 92
DB 25 LEECFRETDEYEFLEAKNGLTATSNPKRVIVGVAGMAGLTAALKLQDAGHTVILEAND 84

QY 93 RVGGRVETVRNKEGMYAEMGAMRIPSSHRIVQVFKLGVEMNEFVMTDDNTFYLVNGV 152
DB 85 RVGGRVETVRNKEGMYAEMGAMRIPSSHRIVQVFKLGVEMNEFVMTDDNTFYLVNGV 142

QY 153 RERTVVOENPDVLKYNVSEKGLSADLLDRLALQKVEEANGCKAALEKYDRYSVK 212
DB 143 RKRGEVNDKPGVLDYVPKPSVSGSAGOLYEEISQKAVEELRRNCTSMYLNKYDTYSTK 202

QY 213 EYLKEEGLSPGAVRMIGDNLNEQSLMTYALSEMIYDQADVNDSTVYHEVTGSGDLLPEA 272
DB 203 EYLLKEGNLSPGAVDMIGDNLNEDSGYVSFIESLKHDDIFAYEKRFEIVGGMDKLTPTS 262

QY 273 FLUSLVDVPIILNSKVKHQRQSKGVIVSYQTGNESSLMDLSADIVLVTTTAKAALFIDFD 329
DB 263 MYQAIQEKVHLNARVIKIQDDVKEVTIVYT-QSEKTLSTVADYIVVCTTSRAARRIKFE 320

QY 330 DFDPLSISKMEALRSVHYDSSTKILLTFRDKFWEDDGIKRGKSTIDGSPSVIYYPSSHPTN 389
DB 321 KFEPELPPKKAHALRSVHYRSGTKIFLTCTKFWEDDGIHGKSTIDGSPSVIYYPSSHPTN 380

QY 390 HTNETIGVLLASYTWSDESLLFLGASDBELKELALRLAKIH---GEQVMDKCTGVIVKWSA 446
DB 381 TSG--VGVIIA-YGIGDDANFFQALDPKOCADIVINDLSLHLPKEDIOFTCHPSMIQR 437

QY 447 WSADPYSLGAFALFTPYQHLEYAQELFSSEGRVHFACEHTAFPHAWTSMKSAIRAAATN 506
DB 438 WSLDKYAMGGITTTPTPYQFQHFSEALTAPVDRIYPAGEYTAQAAGHWIASTIKS 497

QY 507 INKVAEESTIEHTKD 522
DB 498 VNRASENPSTGHLNSD 513

RESULT 9

Q6TQ8 ID Q6TQ8 PRELIMINARY; PRT; 478 AA.
AC Q6TQ8;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE L-amino acid oxidase (fragment).

DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Interleukin-4 induced protein 1 precursor (Fig-1 protein) (mFig1).
 GN Name=1141; Synonyms=Fig1;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/C, and CBA/J;
 RX MEDLINE=97225983; PubMed=9122225; DOI=10.1073/pnas.94.6.2507;
 RA Chu C.C., Paul W.E.;
 RT "Fig1, an interleukin 4-induced mouse B cell gene isolated by cDNA
 RL representational difference analysis.";
 RL Proc. Natl. Acad. Sci. U.S.A. 94:2507-2512(1997).
 RN [2]
 RP SEQUENCE OF 122-289 FROM N.A.
 RC STRAIN=BALB/C; TISSUE=Spleen;
 RX MEDLINE=9901297; PubMed=9798653; DOI=10.1016/S0161-5890(98)00031-5;
 RA Chu C.C., Paul W.E.;
 RT "Expressed genes in interleukin-4 treated B cells identified by cDNA
 RL representational difference analysis.";
 RL Mol. Immunol. 35:487-502(1998).
 RN [3]
 RP SEQUENCE OF 217-630 FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Embryonic head;
 RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
 RA Nikaide I., Otsu N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
 RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojohori T.,
 RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
 RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
 RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
 RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
 RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
 RA Grimmond S., Guscinich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
 RA Kanai A., Kawaji H., Kawasaki Y., Kedzierski R.M., King B.L.,
 RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
 RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
 RA Nagashima T., Nunata K., Okido T., Pavan W.J., Pettea G., Pesole G.,
 RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
 RA Ravasi T., Reed J.C., Reid D.J., Reid J., Ring B.Z., Ringwald M.,
 RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
 RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
 RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
 RA Wilming L.G., Wyehaw-Boris A., Yanagisawa M., Yang I., Yang L.,
 RA Yuan Z., Zavalan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
 RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
 RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
 RA Hara A., Hashizume M., Imotani K., Ishii Y., Itoh M., Kagawa I.,
 RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
 RA Yaeunichi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
 RA Birney E., Hayashizaki Y.;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RL 60,770 full-length cDNAs.";
 RL Nature 420:563-573(2002).
 CC -!- COPACTOR: FAD (Potential).
 CC -!- INDUCTION: By interleukin-4.
 CC -!- SIMILARITY: Belongs to the flavin monooxygenase oxidase family.
 CC Strong, to snake L-amino acid oxidase.

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 CC EMBL; U70429; AAB51353.1; -;
 CC EMBL; U70430; AAB51354.1; -;
 CC EMBL; U89428; AAC36534.1; -;
 CC EMBL; U89429; AAC36535.1; -;

DR EMBL; AK014297; BAB29253.1; ALT_INIT.
 DR HSSD; P81382; 1F8R.
 DR MGD; MG1:109552; 1L411.
 DR InterPro; IPR000759; Adrxn_reductase.
 DR InterPro; IPR001613; Amino_oxidase.
 DR InterPro; IPR002937; Amino_oxidase.
 DR InterPro; IPR000205; NAD_BS.
 DR Pfam; PF01593; Amino_oxidase; 1.
 DR PRINTS; PRO0419; ADXRDTASE.
 DR PRINTS; PRO0757; AMINEOXDASEF.
 KW FAD; Flavoprotein; Oxidoreductase; Signal.
 FT SIGNAL 1 21 Potential.
 FT CHAIN 22 630 Interleukin-4 induced protein 1.
 FT NP_BIND 59 115 FAD (ADP part) (Potential).
 FT CARBOHYD 53 53 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 133 133 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 219 219 N-linked (GlcNAc...) (Potential).
 FT CONFLICT 385 385 R -> Q (in Ref. 3).
 FT CONFLICT 598 630 PSEHVQVHGEVPEWHGHGSGTQPMHVRGDHS -> LRSM
 YRCMGKSSLSGMVGDLPKRCGTGTTNPKKEEVSTOLLS
 QPSSGQTDHLH (in Ref. 3).
 SQ SEQUENCE 630 AA; 70190 MW; A674C5D60D89A071 CRC64;
 Query Match 38.3%; Score 1034; DB 1; Length 630;
 Best Local Similarity 43.5%; Pred. No. 1.7e-55;
 Matches 212; Conservative 100; Mismatches 163; Indels 12; Gaps 6;
 QY 26 ALSLEHLADCLEDDYDTLLQTLQDGLPHINTSHHVIVGVAGMAGLTAAKLLDAGHTV 85
 DB 25 AASSLNPLEKCMEDHDYELLKVVTLGLNRTSKPKQVVVGVAGVAGLVAAKMLSDAGHKV 84
 QY 86 TLEANDRVGRVETRYNEKEGWAEAMGAMRIPSSHRIYVQVFKKLVGEMNEFVMTDDNT 145
 DB 85 TLEADNRIGRIFFREDEKTMGELGAMMPSSHRIHLKLCRTLGLNLTQTYDENT 144
 QY 146 FYLVNGVRETYVQENPDVLYKNVSESEKGISADLLDRLAQKVKKEVEANGCKAALEK 205
 DB 145 WTEVHNKLVNRYVEKMEKGLYNLNNRERGHSPEDIVQMALNKAFKDLKALGCKKAMNK 204
 QY 206 YDRVSVEKYLEEGGLSGAVRMIGDNLNEQSLMYTALSEMIYDQDVNDVSYHYEVTGG 265
 DB 205 FNKHTLLEEGNLSPVOLLGDVMSBGFYLSFAEALRAHACLSRLRYSRIVGG 264
 QY 266 SDLLPEAFSLVDVPIILNSKVGHQKDGKGVISYQTNESLMDLSADIVLVTTAKA 325
 DB 265 WDLPLRALLSSGALLNAPVVSITQGNRVRHIAITSLHSE-KTLTADVLLTASGPA 323
 QY 326 ALFIDFDPLSISKWEALRSVHYDSSTKILLTFRRDKFWEDDGIRGKSIIDGPSRYIYYP 385
 DB 324 LQRTFSPPLTRKQEARLALHYVAASKVFLSFRPPFWHEEHIEGHSNTDRPSRLIYYP 383
 QY 386 SHSFTNETIGVLLASYTMSDESLLFLGASDEBELKELARLDLAKIHGE---QVWDKCTGV 442
 DB 384 ARGEGS-----LLLSYTWSDAAAAPFAGLSLTDQTLRLVLQDVAAHLPPVFLWDG-RGV 437
 QY 443 IVKWSADPYSILGAFALFTPYOHLEYAQELSSSE-GRVHFAGEHTAFPHAWTETSMKSAI 501
 DB 438 -VKRAEDPHSQGGFVQPPPLYGREAEDYDSAPGRIFYFAGEHTALPHGWVETAVKSL 496
 QY 502 RAATNIN 508
 DB 497 RAAVRIN 503
 RESULT 14
 Q6YBV6
 ID Q6YBV6 PRELIMINARY; PRT; 630 AA.
 AC Q6YBV6;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Interleukin-4 induced gene-1 protein.
 GN Name=1141;

OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=WRRL;
RA Chu C.C., Kim J.A., Hsueh K.;
RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY161348; AAC031118.1; -;
DR GO; GO:0016491; P:oxidoreductase activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR000759; Adrndx_reductase.
DR InterPro; IPR001613; Amineoxid fl.
DR InterPro; IPR002937; Amino oxidase.
DR InterPro; IPR000205; NAD BS.
DR Pfam; PF01593; Amino oxidase; 1.
DR PRINTS; PR00419; ADXRDXTASE.
DR PRINTS; PR00757; AMINEOXDASEF.
SQ SEQUENCE 630 AA; 70162 MW; 667515D60D893955 CRC64;

Query Match	38.3%;	Score 1034;	DB 2;	Length 630;
Best Local Similarity	43.5%;	Pred. No. 1.7e-55;		
Matches 212;	Conservative 100;	Mismatches 163;	Indels 12;	Gaps 6;
Qy	26	ALSLSKEHLADCLEDKDYDILQTLNDNGLPHINTSHHVVIVGAGMAGLTAAKLLODAGHTV	85	
Db	25	AASUNLPTEKCMEDHYSQLKVVTLGLNRTSKPKQVVVVGAGVAGVAAKMLSDAGHKV	84	
Qy	86	TILEANDRVGGRVETRYNEKEGWAEKMGAMRIPSSHRIVQFWFKVLGVEMNEFEVMTDNT	145	
Db	85	TILEADNRIGRIITFRDEKTNIGELGAMRMPSSRILHLKRLTGLNLNTQFTQYDENT	144	
Qy	146	FYLVNGVRERTYVVOENPDVLKYNVSESEKISADDDLDRALQVKVBEVEANGKAALEK	205	
Db	145	WTEVHNKVLRYVVEKMPKELGYLNNRERGHSPEDITYQALNKAFXDLKALGCKKAMNK	204	
Qy	206	YDRYSVKEYLKEEGLSPGAVRMTGDLNQLNEOSLMYTALSEMIYQADVNDSVTHVETGG	265	
Db	205	FNKHTLUEYLLEEGNLSPVOLLGDVNMSEEGFFYLSFAEALRAHAACLSDRLSRYIVGG	264	
Qy	266	SDLLPEAPLSVLDVPIILNSVKVHHIROSQDKGIVSYOTGNESSLMDLSADITVLVTTTAKA	325	
Db	265	WDLPLRALLSSLGALLNAPVSIQTGRNDVRVHIATSLHSE-KTITADVVLVLTASGPA	323	
Qy	326	ALFTIDFDPPLSISKWEALRSVHYDSSTKILLTFRDKFWEDDGIRGKSITDGPSRYIYYP	385	
Db	324	LQRITFSPPLTRKQREALRALHYAAAKVLSFRRPFWEHBEHIEGGHSNDRPSSLIFYP	383	
Qy	386	SHSFHTNETIGVLLASVYTSWSDLSLLFGASDEELKEALRDLAKIHGE----QWWDKCTGV	442	
Db	384	AQGEKS-----LLLASVYTSWDAAPFAGLSDTQTLRLVLQVAAALHGVVFLRWDG-RGV	437	
Qy	443	IVKKSADPPYSLGAFALFTPYOHLLEYAQELFSSB-GRVHPAGEHTAGPHAWIETSMKSAI	501	
Db	438	-VKWEADPHSQGFVVQPPPLYGREAEDYDWSAFPGRIYFAGEHTALPHGVMTAVKXSL	496	
Qy	502	RAATNIN	508	
Db	497	RAAVRIN	503	

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RESULT 15
Q6VDI8
ID Q6VDI8 PRELIMINARY; PRT; 630 AA.
AC Q6VDI8;
DT 03-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Interleukin-4 induced gene-1 protein.
GN Name=I4il;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;

```

OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX	NCBI_TaxID=10090;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=NZW;
RA	Chu C.C., Kim J.A., Hsueh K.;
RL	Submitted (Oct-2002) to the EMBL/GenBank/DBJ databases.
RR	EMBL; AY157538; AA017039.1; -.
DR	EMBL; AY157537; AA017038.1; -.
DR	GO; GO:0016491; F:oxidoreductase activity; IEA.
DR	GO; GO:0006118; P:electron transport; IEA.
DR	InterPro; IPR000759; Adrxndx transportase.
DR	InterPro; IPR001613; AminoOxid fl.
DR	InterPro; IPR002937; Amino_oxidase.
DR	InterPro; IPR000205; NAD_5S.
DR	Pfam; PF01593; Amino_oxidase; 1.
DR	PRINTS; PR00419; ADXDRPTASE.
DR	PRINTS; PR00757; AMINEOXDASEF.
SQ	SEQUENCE 630 AA; 70294 MW; 5A90C0CB1B29D9095 CRC64;

Query Match	38.3%	Score 1034	DB 2	Length 630
Best Local Similarity	43.5%	Pred. No. 1.7e-55		
Matches	212	Conservative 100	Mismatches 163	Indels 12
	Gaps			
Qy	26	ALSLKEHLADCLDEKDYDTLLQTLNDGLPHINTSHHVIVVIGAGMAGITAAKLLDAGHTV	85	
Db	25	AASLNPDKMBEDHYEQULKVVTGLNRTSKPKQVVLVVGAGVAGVIAAKMLSDAGHKV	84	
Qy	86	TILEANDRVGRVETVYRNEKEGVAEMGAMRIPSSHRIQVWFVKLGVMNEFWMTDNT	145	
Db	85	TILEADNRIGRIFTFRDEKTMIGELCANRMPSSHRIHLKLCRTGLGNLTQFTQYDNT	144	
Qy	146	FYLVNGVRERTYVQENPDVLKYNVSESEKGISADLLDLRALOKVKEEVEANGKAALEK	205	
Db	145	WTEVHNKLRNVYVEKMPKGLYNLNRERGHSPEDIYQWALNKAFKDLKALGCKKAMNK	204	
Qy	206	YDRYSVKYELKREGGLSPGAVRMIGDLLNQSLMYTALSEMIYDQADVNDSVYTHEVTGG	265	
Db	205	FNKHTLLEYLLEBGNLSRPAQLLGDVWSEEGFYLSFAEALRAHACLSDLRLYSRTVGG	264	
Qy	266	SDLLPEAFSLVDVPIILANSKVKHIRQSDKGVTVSVYQTGNESLMDLSADIVLVTTTAKA	325	
Db	265	WDLPLRALLSSLGALLNAPVSVITQGRNDVZVHATLSLSE-KYLTADVLLTAGSPA	323	
Qy	326	ALFIDEDPPLISIKMBALRSVHVYDSSTKILLTTRDKPWEDDGRGGSRTYIYYP	385	
Db	324	LQRITFSPPLTRKQREALRALHYVAASKVFLSPRRPFWBEHEIEGGHSNDRPSRLIFYP	383	
Qy	386	SHSFHNTNETIGVLLASVTSWSDSLLFLGASDEELKELAPDLAKIHCE---QWMDKCTGV	442	
Db	384	ARGEKS-----LLASVTSWSDAAPFAGLSTDTGLRLVLDQVAALGPPVVFRLWDG-RGV	437	
Qy	443	IVKKWSADPYSLGAFALFPTYQHLEYAQELFSSS-GRVHPFAGBHTAPPFAHIWETSMKSAI	501	
Db	438	-VKRWAEHDHSGQGVVQPLYGREADDYDWSAPFGRIYFAGEHTALPHGWVETAVKSGLI	496	
Qy	502	RAATNIN 508		
Db	497	RAAVRIN 503		

Search completed: October 4, 2005, 14:00:54
Job time : 193 secs

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OM protein - protein search, using sw model

Run on: October 4, 2005, 13:43:40 ; Search time 79 Seconds
(without alignments)
1162.663 Million cell updates/sec

Title: US-10-645-094-1

Perfect score: 2703

Sequence: 1 MNLHVVKWKLVSUVLITLY.....TNINKVANEESTIEHTKDEL 524

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 800245 seqs, 175286397 residues

Total number of hits satisfying chosen parameters: 800245

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending Patents AA New.*

- 1: /cgn2_6/ptodata/2/paa/PCT_NEW_COMB.pcp.*
- 2: /cgn2_6/ptodata/2/paa/US06_NEW_COMB.pcp.*
- 3: /cgn2_6/ptodata/2/paa/US07_NEW_COMB.pcp.*
- 4: /cgn2_6/ptodata/2/paa/US08_NEW_COMB.pcp.*
- 5: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pcp.*
- 6: /cgn2_6/ptodata/2/paa/US10_NEW_COMB.pcp.*
- 7: /cgn2_6/ptodata/2/paa/US11_NEW_COMB.pcp.*
- 8: /cgn2_6/ptodata/2/paa/US60_NEW_COMB.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	999	37.0	567	1	PCT-US03-28361-44
2	999	37.0	567	6	US-10-990-328A-11737
3	999	37.0	567	6	US-10-152-381B-476
4	999	37.0	567	7	US-11-025-607-84
5	407	15.1	478	6	US-10-166-087B-48
6	294	10.9	545	6	US-10-940-774A-11442
7	288	10.7	520	1	PCT-US05-09248-13
8	288	10.7	520	1	PCT-US03-10870-447
9	288	10.7	520	1	PCT-US03-10870-448
10	288	10.7	520	6	US-10-990-328A-8287
11	288	10.7	520	6	US-10-990-328A-8288
12	288	10.7	520	7	US-11-051-454-252
13	283	10.5	527	1	PCT-US05-09248-11
14	283	10.5	527	1	PCT-US03-10870-549
15	283	10.5	527	6	US-10-990-328A-8290
16	283	10.5	527	6	US-10-990-328A-8291
17	283	10.5	527	6	US-10-990-328A-8292
18	283	10.5	527	7	US-11-051-454-250
19	283	10.5	531	6	US-10-940-774A-11443
20	271	10.0	520	1	PCT-US05-11532-1348
21	271	10.0	890	7	US-11-097-143-25362
22	271	10.0	890	7	US-11-097-143-32703
23	263.5	9.7	730	1	PCT-US05-18850-1179
24	252.5	9.3	619	7	US-11-072-512-2472
25	238	8.8	906	6	US-10-450-763-51651

26	229	8.5	527	1	PCT-US03-10870-2456	Sequence 2456, Ap
27	221	8.2	513	6	US-10-218-141-1224	Sequence 1224, Ap
28	221	8.2	518	6	US-10-218-141-3192	Sequence 3192, Ap
29	220.5	8.2	583	7	US-11-097-143-17742	Sequence 17742, A
30	218.5	8.1	448	1	PCT-IB03-06509-4659	Sequence 4659, Ap
31	218.5	8.1	448	6	US-10-934-893-4659	Sequence 4659, Ap
32	205	7.6	558	6	US-10-501-098-1	Sequence 1, Appl
33	196.5	7.3	509	7	US-11-097-143-17202	Sequence 17202, A
34	187	6.9	502	7	US-11-097-143-42648	Sequence 42648, A
35	183.5	6.8	500	6	US-10-471-571A-3712	Sequence 3712, Ap
36	181.5	6.7	503	6	US-10-914-020-7202	Sequence 7202, Ap
37	175.5	6.5	421	6	US-10-501-098-2	Sequence 2, Appl
38	173	6.4	511	6	US-10-504-601-6	Sequence 6, Appl
39	173	6.4	511	6	US-10-152-381B-122	Sequence 122, App
40	170.5	6.3	504	6	US-10-504-601-4	Sequence 4, Appl
41	169.5	6.3	479	7	US-11-097-143-12792	Sequence 12792, A
42	169	6.3	502	6	US-10-471-571A-3706	Sequence 3706, Ap
43	166	6.1	476	7	US-11-097-143-11910	Sequence 11910, A
44	165.5	6.1	484	6	US-10-914-020-7130	Sequence 7130, Ap
45	165.5	6.1	512	7	US-11-100-328-19	Sequence 19, Appl

ALIGNMENTS

RESULT 1

PCT-US03-28361-44

; Sequence 44, Application PC/TUS0328361

; GENERAL INFORMATION:

; APPLICANT: GENENTECH, INC.

; APPLICANT: SARAH C. BODARY

; APPLICANT: HILARY CLARK

; APPLICANT: BRISDELL HUNTE

; APPLICANT: JANET K. JACKMAN

; APPLICANT: JILL SCHOENFELD

; APPLICANT: P. MICKY WILLIAMS

; APPLICANT: WILLIAM I. WOOD

; APPLICANT: THOMAS D. WU

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TREATMENT OF IMMUNE

; FILE OF INVENTION: RELATED DISEASES

; FILE REFERENCE: P1975R1-PCT

; CURRENT APPLICATION NUMBER: PCT/US03/28361

; PRIOR FILING DATE: 2003-09-10

; PRIOR APPLICATION NUMBER: US 60/410,174

; PRIOR FILING DATE: 2002-09-11

; NUMBER OF SEQ ID NOS: 104

; SEQ ID NO 44

; LENGTH: 567

; TYPE: PRT

; ORGANISM: Homo sapiens

PCT-US03-28361-44

Query Match 37.0%; Score 999; DB 1; Length 567;
Best Local Similarity 41.8%; Pred. No. 1.4e-65;
Matches 217; Conservative 99; Mismatches 171; Indels 32; Gaps 9;

Qy	3	LHVVKWKLVSUVLITLYSHT-VALSKHLEADCLDKDYDTLLQTLNDGLPHINTSHH	61
Db	6	LHL-----LVLPILLSVASQDWKAERSQDPFKMOPDYEQLLVKVVTVGNLTLKPQR	61
Qy	62	VVIIVGAGMAGLTAAKLLQDAGHTVTILEANDRVGGRVETRYNEKEGWYAEMGAMRIPSSH	121
Db	62	VIVVAGVAGVLAALKVLSAGHKVTILEADNRIGGRIFTYRDQNTGWIGELGAMRMPSSH	121
Qy	122	RIVQWFVKVLGVENEFVMTDDNTFYLVNGVRETYVQVNPDLVKYVNSEKISADD	181
Db	122	RILHLKQGLGLNLTFTQYDKNTWTEVHEKLYNVYVVEKPEKLGVALRPOEKHSPED	181
Qy	182	LLDLALQKVEEVEANGCKALEKYDYRYVKEYLKESGSLSPGAVRMTGLDNLNEOSLMT	241
Db	182	IYQNALQALDKALCGRKAMKPFERHTLLELLYLLGEGNLSRPVQLLLGDVMSDEGFFYL	241
Qy	242	ALSEMIYDQADVNDVSVTYHEVTGSGDLLPEAFLSVLDVPIILLNSKVKHQRSKGVISVY	301

Qy	361	KFWEDDGI	RCKSIT	DGSPSR	IYYP	PSHSFHT	NETICV	LASWTW	DESLLF	GASDEUK	420
		:::::	:	:	:	:	:	:	:	:	
Db	362	PFWREEH	JEGHSN	TDRSMR	IFYP-	----	PPREGA	LLASYT	SDAAAAF	AGLSREAL	416
		:::::	:	:	:	:	:	:	:	:	
Qy	421	ELALRD	LAKING	-EQWMD	KCTGV	VKKWSAD	PYVQ	HLEAQE	LFSS-	476	
		:::::	:	:	:	:	:	:	:	:	
Db	417	RLALDD	VVAALH	GPVRQL	WDG-TG	VKRWAED	QHSGGF	VVPQP-	-----	ALWOTEK	466
		:::::	:	:	:	:	:	:	:	:	
Qy	477	-----	GRVPHAGE	HTAFP	HIAWI	ETSMKS	AIRAAT	NNIN	508		
		:::::	:	:	:	:	:	:	:	:	
Db	467	DDWTVPG	RIYFA	GEHTAY	PHGWVB	TAVKSA	LRAAIK	IN	505		
		:::::	:	:	:	:	:	:	:	:	

RESULT 4
US-11-025-607-84
; Sequence 84, Application US/11025607
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Botstein, David
; APPLICANT: Deenoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same

```

; FILE REFERENCE: P2830P1C1
; CURRENT APPLICATION NUMBER: US/11/025,607
; CURRENT FILING DATE: 2004-12-28
; PRIOR APPLICATION NUMBER: US/09/946,374
; PRIOR FILING DATE: 2001-09-04
; PRIOR APPLICATION NUMBER: 60/098716
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098723
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098749
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098750
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098803
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098821
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098843
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/099536
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099596
; PRIOR FILING DATE: 1998-09-09
; Remaining prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 84
; LENGTH: 567
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-025-607-84

```

[illegible]

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RESULT 5
US-10-166-087B-48
; Sequence 48, Application US/10166087B
; GENERAL INFORMATION:
; APPLICANT: Ecopia Biosciences Inc.
; APPLICANT: Farnet, Chris
; APPLICANT: Staffa, Alfredo
; APPLICANT: Zazopoulos, Emmanuel
; TITLE OF INVENTION: NUCLEIC ACID
; TITLE OF INVENTION: ANTHRAMYCIN
; FILE REFERENCE: 3014-2US
; CURRENT APPLICATION NUMBER: US/10/166,087B
; CURRENT FILING DATE: 2002-06-11
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn version 3.0
; SEQ. ID. NO 48
; LENGTH: 478
; TYPE: PRT
; ORGANISM: Streptomyces refuineus subspecies thermotolerans
US-10-166-087B-48

```

Query Match	15.1%	Score 407;	DB 6;	Length 478;
Best Local Similarity	29.2%;	Pred. No. 7.5e-22;		
Matches 144;	Conservative 83;	Mismatches 196;	Indels 70;	Gaps 20;
Qy	47	QTLNGLPHINTSHHVIVVIGAGMAGTAAKLLQDAGHTVTLLEANDVGGRVETRYNE-K 105		
Db	11	ETFDSIPQHGTSVVIVGAGLAGLAAAHLETRQGVTVTVLEADSPGGRTWTLREPPA 70		
Qy	106	EGHYAEMGAMRIPSSHRIIVQVFVKKLGVENNEFMTDDNTFYLVNGVRYRTYVYVQBNPDV 165		
Db	71	DGLRAAGAMTVTEHCHYTHMYLKEHGIGTEPSDLVDTDFGYHRNGVRIPDPKVGGEHADL 130		

Db 315 MIIDGEEAPVAYTLDDTKPEGNYAA--IMGFILAHHKARKLARL-----TKBERLKKLCELY 368
Qy 423 -----ALRDLAKIHGEQWMDKCTGTVIVKKWSADPYSLGAFALFTPYQHL-EYAQELFSSE 476
Db 369 AKVLGSLEALEPVHYEE-----KNWCEEQYSGGCYTYFPFGILTYQGRVLRQPV 418
Qy 477 GRVHFAGHTAPPH--AWIETSMKSAIRAATNI-----NKVANE 514
Db 419 DRIYFAGTETA-THWSGYMEGAVEAGEARAAREILHAMGKIPED 461

RESULT 8

PCT-US03-10870-447
; Sequence 447, Application PC/TUS0310870
; GENERAL INFORMATION:
; APPLICANT: Mitokor, Inc.
; APPLICANT: Buck Institute
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Fahy, Boin D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Warnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; FILE REFERENCE: 660088.465PC
; CURRENT APPLICATION NUMBER: PCT/US03/10870
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3025
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 447
; LENGTH: 520
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US03-10870-447

Query Match 10.7%; Score 288; DB 1; Length 520;
Best Local Similarity 25.0%; Pred. No. 5.4e-13;
Matches 131; Conservative 84; Mismatches 169; Indels 140; Gaps 27;
Qy 62 VVIVGAGMAGLTAAKLQDAGHTVILEANDRVGRVETRYNEKEGWAEMGAMRI-PSS 120
Db 7 VVVGGGSGMAAAKLLHDSGLNVVLEARDVGRGRTYTLRNQKVK-YVDLGGSYVGPTQ 65
Qy 121 HRIVQWFKVLGVE---MNEFVMTDDNTFYLNGVRERTYVVOE-----NPDVLKYNVS 171
Db 66 NRILR-LAKELGLEYKYNEVER-----LIHHVKGKSYPPRGPFPVWNP--ITY--- 112
Qy 172 ESEKISADDDLLD-----RALQKVEEVEANG-CKAAL-EKYDRYSVKEYLKEEGLSPG 224
Db 113 -----LDHNNFWRTDDMGREIPSDAPWKAPLAEEDWNTMKELL----- 152
Qy 225 AVRMIGDLLNEOSLMYTALSEMIYDQADVNSVT--YHEVT----- 263
Db 153 -----DKLCWTESAKQL-ATLFVNLVCVTAETHEVSALWFLWYVKQCGGTTTIIIS 200
Qy 264 -----GGSDLLPEAFSLVDVPILLNSKVKHRSQDKGVIVSYQTGNESSLMDL 312
Db 201 TTNGQERKFVGGSGQVSEIRIMDLGDRVKLERPVIYIDQTRNVLV--ETLNHEM---Y 255
Qy 313 SADVILVTAKAALFIDPPLPSISKMEALRSVHYDSSTKILLTFRDKFWEDDGIIRGK 372
Db 256 EAKYVISAIPPTLGMKIHFNPLPMRNQMITRVLGSLGVKICIVYKPFWRKKDY-CGT 314
Qy 373 SITDGPSRYIY-----PSHSFHTNETIGVLLASYSWTSDSLLFLGASDEBKEL---- 422
Db 315 MIIDGEEAPVAYTLDDTKPEGNYAA--IMGFILAHHKARKLARL-----TKBERLKKLCELY 368
Qy 423 -----ALRDLAKIHGEQWMDKCTGTVIVKKWSADPYSLGAFALFTPYQHL-EYAQELFSSE 476
Db 369 AKVLGSLEALEPVHYEE-----KNWCEEQYSGGCYTYFPFGILTYQGRVLRQPV 418

RESULT 10

Qy 477 GRVHFAGHTAPPH--AWIETSMKSAIRAATNI-----NKVANE 514
Db 419 DRIYFAGTETA-THWSGYMEGAVEAGEARAAREILHAMGKIPED 461

RESULT 9

PCT-US03-10870-448
; Sequence 448, Application PC/TUS0310870
; GENERAL INFORMATION:
; APPLICANT: Mitokor, Inc.
; APPLICANT: Buck Institute
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Fahy, Boin D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Warnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; FILE REFERENCE: 660088.465PC
; CURRENT APPLICATION NUMBER: PCT/US03/10870
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3025
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 448
; LENGTH: 520
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US03-10870-448

Query Match 10.7%; Score 288; DB 1; Length 520;
Best Local Similarity 25.0%; Pred. No. 5.4e-13;
Matches 131; Conservative 84; Mismatches 169; Indels 140; Gaps 27;
Qy 62 VVIVGAGMAGLTAAKLQDAGHTVILEANDRVGRVETRYNEKEGWAEMGAMRI-PSS 120
Db 7 VVVGGGSGMAAAKLLHDSGLNVVLEARDVGRGRTYTLRNQKVK-YVDLGGSYVGPTQ 65
Qy 121 HRIVQWFKVLGVE---MNEFVMTDDNTFYLNGVRERTYVVOE-----NPDVLKYNVS 171
Db 66 NRILR-LAKELGLEYKYNEVER-----LIHHVKGKSYPPRGPFPVWNP--ITY--- 112
Qy 172 ESEKISADDDLLD-----RALQKVEEVEANG-CKAAL-EKYDRYSVKEYLKEEGLSPG 224
Db 113 -----LDHNNFWRTDDMGREIPSDAPWKAPLAEEDWNTMKELL----- 152
Qy 225 AVRMIGDLLNEOSLMYTALSEMIYDQADVNSVT--YHEVT----- 263
Db 153 -----DKLCWTESAKQL-ATLFVNLVCVTAETHEVSALWFLWYVKQCGGTTTIIIS 200
Qy 264 -----GGSDLLPEAFSLVDVPILLNSKVKHRSQDKGVIVSYQTGNESSLMDL 312
Db 201 TTNGQERKFVGGSGQVSEIRIMDLGDRVKLERPVIYIDQTRNVLV--ETLNHEM---Y 255
Qy 313 SADVILVTAKAALFIDPPLPSISKMEALRSVHYDSSTKILLTFRDKFWEDDGIIRGK 372
Db 256 EAKYVISAIPPTLGMKIHFNPLPMRNQMITRVLGSLGVKICIVYKPFWRKKDY-CGT 314
Qy 373 SITDGPSRYIY-----PSHSFHTNETIGVLLASYSWTSDSLLFLGASDEBKEL---- 422
Db 315 MIIDGEEAPVAYTLDDTKPEGNYAA--IMGFILAHHKARKLARL-----TKBERLKKLCELY 368
Qy 423 -----ALRDLAKIHGEQWMDKCTGTVIVKKWSADPYSLGAFALFTPYQHL-EYAQELFSSE 476
Db 369 AKVLGSLEALEPVHYEE-----KNWCEEQYSGGCYTYFPFGILTYQGRVLRQPV 418
Qy 477 GRVHFAGHTAPPH--AWIETSMKSAIRAATNI-----NKVANE 514
Db 419 DRIYFAGTETA-THWSGYMEGAVEAGEARAAREILHAMGKIPED 461

```
US-10-990-328A-8287
; Sequence 8287, Application US/10990328A
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; TITLE OF INVENTION: POLYMORPHISMS IN NUCLEIC ACID MOLECULES
; TITLE OF INVENTION: ENCODING HUMAN ENZYME PROTEINS, METHODS OF DETECTION AND
; FILE REFERENCE: CL001495
; CURRENT APPLICATION NUMBER: US/10/990,328A
; CURRENT FILING DATE: 2004-11-17
; NUMBER OF SEQ ID NOS: 558824
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8287
; LENGTH: 520
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-990-328A-8287

Query Match      10.7%; Score 288; DB 6; Length 520;
Best Local Similarity 25.0%; Pred. No. 5.4e-13;
Matches 131; Conservative 84; Mismatches 169; Indels 140; Gaps 27;

QY 62 VVIVAGMAGLTAAKLLQDAGHTVTLLEANDRVGRVETYNEXEGVYAENGAMRI-PSS 120
Db 7 VVVVGGGSGMAAAKLLHDSGLNVVLEARDRVGGRVTLRNQKVK-YVDLGGSYVGPTQ 65
QY 121 HRIQWQFVKLGVE---MNEFVMTDDNTFYLVNGVRERTYVVOE-----NPDVLKYNVS 171
Db 66 NRILR-LAKELGLETYKNEVER-----LIHHVKGKSYPRGPPFPVWNP--ITY--- 112
QY 172 ESEKGISADDLLD-----RALQKVEEVEANG-CKAAL-EKYDRYSVKYEYLKEEGLSPG 224
Db 113 -----LDHNNFWRTWDDMGREIPSDAPWKAPLAEWDNMTMKELL----- 152
QY 225 AVRMTGDLNQLSEMYTALSEMIYQDADVNSVT--YHEVT----- 263
Db 153 -----DKLCWTESAKQL-ATLFVNLCVTAETHEVSALWFLWYVKQCGGTTIRIS 200
QY 264 -----GSDLLPEAFSLVDVPIILLNSKVKHQSDKGVIYSYQTNESLMDL 312
Db 201 TTNGQERKRVGGSGQVSEIMDLGDRVKLERPVYIDQRENVLV--ETLNHEM---Y 255
QY 313 SADIVLVTTTAKAALFIDFPPLSLISKMEALRSVHYDSSTKILLTFRDKFWEDDGIROGK 372
Db 256 EAKYVISAIPPTLGMKIHFNPPLPMRNQMITRVLPSGVKICVYVYKEPFWKXKDY-CGT 314
QY 373 SITDGPRIYY-----PSHSFHTNETIGVLLASYTWSDESLLPLGASDEBELKEL----- 422
Db 315 MIIDGEEAPVAYTLDDTKPEGNYAA--IMGFILAHKARKLARL-----TKEERLKKLCBLY 368
QY 423 -----ALRDLAKIHGEQVWDKCTGIVVKWSADPYSLGAFALFTPYQHL-EYAOELFSSE 476
Db 369 AKVLGSLALEPVHYEE-----KNWCEEQYSGGCYTTYPFGILTOYGRVLRQPV 418
QY 477 GRVHFAGEHTAPPH--AWIETSMKSAIRAATNI----NKVANE 514
Db 419 DRIYFAGTETA--THWSGYMEGAVEAGERAAREILHAMGKIPED 461

RESULT 11
US-10-990-328A-8288
; Sequence 8288, Application US/10990328A
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; TITLE OF INVENTION: POLYMORPHISMS IN NUCLEIC ACID MOLECULES
; TITLE OF INVENTION: ENCODING HUMAN ENZYME PROTEINS, METHODS OF DETECTION AND
; FILE REFERENCE: CL001495
; CURRENT APPLICATION NUMBER: US/10/990,328A
; CURRENT FILING DATE: 2004-11-17
; NUMBER OF SEQ ID NOS: 558824
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8288
; LENGTH: 520
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-990-328A-8288

Query Match      10.7%; Score 288; DB 6; Length 520;
Best Local Similarity 25.0%; Pred. No. 5.4e-13;
Matches 131; Conservative 84; Mismatches 169; Indels 140; Gaps 27;

QY 62 VVIVAGMAGLTAAKLLQDAGHTVTLLEANDRVGRVETYNEXEGVYAENGAMRI-PSS 120
Db 7 VVVVGGGSGMAAAKLLHDSGLNVVLEARDRVGGRVTLRNQKVK-YVDLGGSYVGPTQ 65
QY 121 HRIQWQFVKLGVE---MNEFVMTDDNTFYLVNGVRERTYVVOE-----NPDVLKYNVS 171
Db 66 NRILR-LAKELGLETYKNEVER-----LIHHVKGKSYPRGPPFPVWNP--ITY--- 112
QY 172 ESEKGISADDLLD-----RALQKVEEVEANG-CKAAL-EKYDRYSVKYEYLKEEGLSPG 224
Db 113 -----LDHNNFWRTWDDMGREIPSDAPWKAPLAEWDNMTMKELL----- 152
QY 225 AVRMTGDLNQLSEMYTALSEMIYQDADVNSVT--YHEVT----- 263
Db 153 -----DKLCWTESAKQL-ATLFVNLCVTAETHEVSALWFLWYVKQCGGTTIRIS 200
QY 264 -----GSDLLPEAFSLVDVPIILLNSKVKHQSDKGVIYSYQTNESLMDL 312
Db 201 TTNGQERKRVGGSGQVSEIMDLGDRVKLERPVYIDQRENVLV--ETLNHEM---Y 255
QY 313 SADIVLVTTTAKAALFIDFPPLSLISKMEALRSVHYDSSTKILLTFRDKFWEDDGIROGK 372
Db 256 EAKYVISAIPPTLGMKIHFNPPLPMRNQMITRVLPSGVKICVYVYKEPFWKXKDY-CGT 314
QY 373 SITDGPRIYY-----PSHSFHTNETIGVLLASYTWSDESLLPLGASDEBELKEL----- 422
Db 315 MIIDGEEAPVAYTLDDTKPEGNYAA--IMGFILAHKARKLARL-----TKEERLKKLCBLY 368
QY 423 -----ALRDLAKIHGEQVWDKCTGIVVKWSADPYSLGAFALFTPYQHL-EYAOELFSSE 476
Db 369 AKVLGSLALEPVHYEE-----KNWCEEQYSGGCYTTYPFGILTOYGRVLRQPV 418
QY 477 GRVHFAGEHTAPPH--AWIETSMKSAIRAATNI----NKVANE 514
Db 419 DRIYFAGTETA--THWSGYMEGAVEAGERAAREILHAMGKIPED 461

RESULT 12
US-11-051-454-252
; Sequence 252, Application US/11051454
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Endege, Wilson O.
; APPLICANT: Gannavarapu, Manjula
; APPLICANT: Gorbacheva, Bella
; APPLICANT: Hoersch, Sebastian
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Wonsey, Angela M.
; APPLICANT: Glatt, Karen
; APPLICANT: Zhao, Xumei
; APPLICANT: Anderson, Dustin
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF PROSTATE CANCER
; FILE REFERENCE: MRI-044
; CURRENT APPLICATION NUMBER: US/11/051,454
; CURRENT FILING DATE: 2005-02-04
; PRIOR APPLICATION NUMBER: US/10/205,823
; PRIOR FILING DATE: 2002-07-25
; PRIOR APPLICATION NUMBER: 60/307,982
; PRIOR FILING DATE: 2001-07-25
; PRIOR APPLICATION NUMBER: 60/314,356
; PRIOR FILING DATE: 2001-08-22
```

; PRIOR APPLICATION NUMBER: 60/325,020
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: 60/341,746
; PRIOR FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: 60/362,158
; PRIOR FILING DATE: 2002-03-05
; NUMBER OF SEQ ID NOS: 455
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 520
; LENGTH: 520
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-051-454-252

Query Match 10.7%; Score 288; DB 7; Length 520;
Best Local Similarity 25.0%; Pred.No.5.4e-13;
Matches 131; Conservative 84; Mismatches 169; Indels 140; Gaps 27;

Qy 62 VVIVGAGMAGLITRAKLLODAGHTVTILEANDRVGRGVETRYRNEKEGYAEMGAMRI-PSS 120
Db |||:|||||||:|||||||:|||||||:|||||||:|||||||:|||||||:|||||||:
7 VVVVGGSIGMAAKLLHDSGLNVVLEARDVRGGRTYTLRNQKV-YVDLGSGSYVGPQTQ 65
Qy 121 HRTVOWPVKLGVE---MNFEFMTDDNTFYLVNGVRERTYVQE-----NPDVLKNYS 171
Db |||:|||||||:|||||||:|||||||:|||||||:|||||||:|||||||:|||||||:
66 NRILUR-LAKEGLUETYKNEVER-----LIHHVKGSYPFRPPFPWNP--ITY--- 112
Qy 172 ESEKGISADLLD-----RALQVKBEVEANG-CKAAL-EKYDRYSVKVELKEEGGLSPG 224
Db |||:|||||||:|||||||:|||||||:|||||||:|||||||:|||||||:|||||||:
113 -----LDHNPNFWRTMDDMGREIPSDAPWKAPLAEEWDNMTKELL----- 152
Qy 225 AVRMIGDLLNEQSIMTYALSEMITYDOADVNSVT--YHEVT----- 263
Db |||:|||||||:|||||||:|||||||:|||||||:|||||||:|||||||:|||||||:
153 -----DKLCWTESAKQL-ATLFVNLCVTAETHVSALWFELVYVKQCQGTTTIFS 200
Qy 264 -----CGSDDLPEAFSLVDPTILLNSKVKHIRSQDGVIIVSVOTGNESLMDL 312
Db |||:|||||||:|||||||:|||||||:|||||||:|||||||:|||||||:|||||||:
201 TTNGGQRKFVGGSGQVSEIRIMDLGDGRVKLERPIVIDOTRENVLV--ETLNHEM---Y 255
Qy 313 SADIVLVTTAKAALFTDFPPLISIKMEALRSVHYDSSTKILLTPRDKFWBDDGIRGGK 372
Db |||:|||||||:|||||||:|||||||:|||||||:|||||||:|||||||:|||||||:
256 EAKYVISAIPTLGMKIHFNPPLPMNRNQMITVPPLSGSVIKCIYYKEFPWRKKDY-CGT 314
Qy 373 SITDGSERYIYY-----PSHSFHTNETIGVLASVYWSDSELFLFGASDEELKEI---- 422
Db |||:|||||||:|||||||:|||||||:|||||||:|||||||:|||||||:|||||||:
315 MIIDGSEAPVAYTLDDTKPEGNVAA--IMGFILAHKARKLARL---TKEERLKXLCLEY 368
Qy 423 -----ALRDALKTHGEQVWDKCTGVIVKWSADPYSLGAFALFTPVOHL-EYAQELFSSE 476
Db |||:|||||||:|||||||:|||||||:|||||||:|||||||:|||||||:|||||||:
369 AKVLGSLALEPHVHYEE-----KNWCBEQSGCYTTYFFPGGILTQYGRVLRQP 418
Qy 477 GRVHFAGENTAPPH--AWIETSMSKAIRAATNI---NKVANEE 514
Db |||:|||||||:|||||||:|||||||:|||||||:|||||||:|||||||:|||||||:
419 DRIYFAGTETA-THWSGYMEGAEGAARAAREILHAMGKIPED 461

RESULT 13
PCT-US05-09248-11
; Sequence 11, Application PC/TUS0509248
; GENERAL INFORMATION:
; APPLICANT: Xu, Jianchao
; APPLICANT: Desir, Gary
; TITLE OF INVENTION: DETECTION, ISOLATION AND USES OF RENALASE (MONOAMINE OXIDASE C)
; FILE REFERENCE: 044574-5133-WO
; CURRENT APPLICATION NUMBER: PCT/US05/09248
; CURRENT FILING DATE: 2005-03-28
; PRIOR APPLICATION NUMBER: US 60/554,552
; PRIOR FILING DATE: 2004-03-19
; PRIOR APPLICATION NUMBER: US 60/615,452
; PRIOR FILING DATE: 2004-10-01
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 11
; LENGTH: 527

Matches	121;	Conservative	91;	Mismatches	197;	Indels	108;	Gaps	18;
Qy	62	VVIVGAGMAGLTAALKLODAGHTVTILEANDRVGGRTYRNEKEGVYAENGAMRIPISSH	121						
Db	16	VWVGIGSIGLSAAKLLTEVGSVLVLARDRDVGGRVTYIRNEHVVDYDVGVAVGPTQN	75						
Qy	122	RIVQVFVKILGVEMFEFMTDDNTFYLVNGVRERYVVOE-----NP-DVLKNVSESE	174						
Db	76	RILR-LSKELGIETYKVNVSE----RLVQYVKGKTYPRFGAPPPVMNPIAYLDYN----	125						
Qy	175	KGISADDLLDRALOKVEEVEANGCKAA--LEKYDRYSVKEYLKEEGGLSPCAVRMIGDL	232						
Db	126	-----NLWRITIDNMGKEIPTDAPEAQHADKWDKMTKE-----L	160						
Qy	233	LNEQSMLMYTALSEMIYDAQDNDSVTYHEVT-----	263						
Db	161	IDKICWTKTA-RRFAYFLVNINVTSPHESVALFWLVVKKVCGGTTRIFSVTNGQBERKF	219						
Qy	264	-GGSDLLPAFLSLVDVPILLNKVKHIQSDKGVIVSVQTGNESLLMDLADIVLVTTT	322						
Db	220	VGSGQVSERIMDLLGGQVKLNHPVTHVQSSDNIIE-TLNHEHYECKYVINAIPLTL	278						
Qy	323	AKAALFIDFPPLSISKMBALRSVHYDSSSTKILLTRFDKFWEDDGIRGCKSITDPGRYI	382						
Db	279	AK-----IHRFPELPAERNQLIQRLPNGAVIKCMYYKCAFKKDKYCCGMIIEDDAPI-	333						
Qy	383	YYPSSHFTNET-----IGULLASTWSDESLLFLGASDEBELKELARDL-AKIHG	432						
Db	334	-----SITLDDTKPFGSLPAIMGFIARLK--ADR-----LAKLHKIRKKKICELYAKVLG	382						
Qy	433	EQVWDKCTGVIVKKSADPVSLGAF-ALFTPYOHLLEYAQLFSSBGRVHFAGEHTA----	487						
Db	383	SQBALHPVHYEEKWCNEEQYSGCYTAYPPGIMTQYGRVIRQPVGRIFFAGTATATKWS	442						
Qy	488	-FPHAMIETSMKSIRAIRANTINKVANEESTIBHTKDE	523						
Db	443	GYMEGAVEACERAAREVLNGLGKVKTEKDIIWVQBPESK	479						
RESULT 15									
US-10-990-328A-8290									
; Sequence 8290, Application US/10990328A									
; GENERAL INFORMATION:									
; APPLICANT: CARGILL, Michele									
; TITLE OF INVENTION: POLYMORPHISMS IN NUCLEIC ACID MOLECULES									
; TITLE OF INVENTION: ENCODING HUMAN ENZYME PROTEINS, METHODS OF DETECTION AND									
; FILE REFERENCE: CL001495									
; CURRENT APPLICATION NUMBER: US/10/990,328A									
; CURRENT FILING DATE: 2004-11-17									
; NUMBER OF SEQ ID NOS: 558824									
; SOFTWARE: FastSeq for Windows Version 4.0									
; SEQ ID NO 8290									
; LENGTH: 527									
; TYPE: PRT									
; ORGANISM: Homo sapiens									
US-10-990-328A-8290									

```

Qy 233 LNEOSLWYLTALSEMIYOADVNDVSYYHEVT----- 263
Db 161 IDKICTWKTA--RRFAYLFVNINVTSEPEVALFWLVYKQCGRTRIFSVTNGGOERKF 219
Qy 264 -GGSDLLPEAFSLVDLPILLANSKVKHIRQSDDKGVIYSQTGNESLMDSLDSADVLTUTT 322
Db 220 VGGSGQVSERIMDLGLDGVKLHPHVVHQSSDNIIIE-TLNHEHYECKYVINAIPTTUT 278
Qy 323 AKAAALFDIDFPPLSTISKEALRSVHYDSSTIKLLTFRDKFWEDDGIIRGCKSITDGPSRYI 382
Db 279 AK----IHFRELPARNQLQRUPMGAVIKCMYYKEAFAWKDDYCGCMIIEDEDAP I- 333
Qy 383 YYPHSFHTNET-----IGULLASYTWSDESLLFLGHASDEBELKELARDL-AKING 432
Db 334 ----SITLDDTKPDGSLPAIMGFTLRK--ADR----LAKLHKIRKKKICELYAKVLG 382
Qy 433 EQVWDKCTGVIVKKSADDPYSLGAF-ALFTPVPQHLEYAQELFSSRGRVHFAGEHTA--- 487
Db 383 SQEALHPVHYEEKWCBEQYSGGCYTATPPGIMTQYGRVKIPQVRIFPAGTETATKWS 442
Qy 488 -FPHAWIETSMKSIRAATNINKVANEESTIEHTKDE 523
Db 443 GYMEGAVEAGERAREVLNGLKYTEKEDIWVOEPESK 479

Search completed: October 4, 2005, 13:57:37
Job time : 81 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 4, 2005, 13:47:25 ; Search time 166 Seconds
(without alignments)
1220.858 Million cell updates/sec

Title: US-10-645-094-1

Perfect score: 2703

Sequence: 1 MNLHVWVKLSVSVSLITLY.....TNINKVNEESTIEHTKDEL 524

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

- 1: Geneseqp1980s:*
- 2: Geneseqp1990s:*
- 3: Geneseqp2000s:*
- 4: Geneseqp2001s:*
- 5: Geneseqp2002s:*
- 6: Geneseqp2003as:*
- 7: Geneseqp2003bs:*
- 8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2703	100.0	524	2	AAW96805
2	1048.5	38.8	523	8	ADO60382
3	1034	38.3	630	5	ABB10103
4	999	37.0	567	2	AAW75770
5	999	37.0	567	2	AAV06480
6	999	37.0	567	3	AAV99364
7	999	37.0	567	3	AAV93687
8	999	37.0	567	4	AAAB66113
9	999	37.0	567	4	AAV72874
10	999	37.0	567	4	AAAB50962
11	999	37.0	567	4	AAU12409
12	999	37.0	567	5	ABB84904
13	999	37.0	567	5	ABB10104
14	999	37.0	567	5	ABB95510
15	999	37.0	567	6	ABO17853
16	999	37.0	567	6	ADA56835
17	999	37.0	567	6	ABU81107
18	999	37.0	567	6	ABU71428
19	999	37.0	567	6	ABU66807
20	999	37.0	567	6	ADA40686
21	999	37.0	567	6	ABR47699
22	999	37.0	567	6	ABU59888
23	999	37.0	567	6	ABG74758
24	999	37.0	567	6	ABO25078
25	999	37.0	567	6	ABU67083

26	999	37.0	567	6	ADA45995	Ada45995	Novel hum
27	999	37.0	567	6	ADA76426	Ada76426	Human PRO
28	999	37.0	567	6	ADA19076	Ada19076	Human PRO
29	999	37.0	567	6	ADA61699	Ada61699	Homo sapi
30	999	37.0	567	6	ADB19484	ADB19484	Novel hum
31	999	37.0	567	6	ADB28025	ADB28025	Human PRO
32	999	37.0	567	6	ADA86504	ADA86504	Novel hum
33	999	37.0	567	6	ADB16068	ADB16068	Human PRO
34	999	37.0	567	6	ADA47854	ADA47854	Human PRO
35	999	37.0	567	6	ABO33606	ABO33606	Novel hum
36	999	37.0	567	6	ADA67649	ADA67649	Human PRO
37	999	37.0	567	6	ADB30656	ADB30656	Human PRO
38	999	37.0	567	6	ADA85952	ADA85952	Novel hum
39	999	37.0	567	6	ADA97164	ADA97164	Human PRO
40	999	37.0	567	6	ADA79468	ADA79468	Human PRO
41	999	37.0	567	6	ADA87607	ADA87607	Novel hum
42	999	37.0	567	6	ADB16809	ADB16809	Human PRO
43	999	37.0	567	6	ADA91901	ADA91901	Novel hum
44	999	37.0	567	6	ADB14964	ADB14964	Human PRO
45	999	37.0	567	6	ADB18925	ADB18925	Novel hum

ALIGNMENTS

RESULT 1

AAW96805
ID AAW96805 standard; protein; 524 AA.

AC AAW96805;

DT 23-APR-1999 (first entry)

DE An apoptosis inducing protein.

XX Cell death; apoptosis; inhibition; proliferation; cancer cell;
apoptosis inducing protein; AIP; chub mackerel; anticancer.

OS Scomber japonicus.

PN WO9852972-A1.

PD 26-NOV-1998.

PF 22-MAY-1998; 98WO-JP002261.

PR 23-MAY-1997; 97JP-00133549.

XX (TENS-) TENSEI SUISAN CO LTD.

XX Iwamoto M, Jung S;

XX WPI; 1999-070139/06.

DR N-ESDB; AAX15122.

PT Apoptosis inducing protein from mackerel and gene encoding it - for use
as anticancer agents.

XX Claim 1; Page 30-31; 47pp; Japanese.

PS The present sequence represents a protein which induces cell death
(apoptosis) and inhibits the proliferation of cancer cells. The protein
CC (apoptosis) inducing protein, AIP) is isolated from chub mackerel. The
protein can be used as an anticancer agent and as a reagent for study of
the mechanisms of apoptosis in vitro

XX Sequence 524 AA;

Query Match 100.0%; Score 2703; DB 2; Length 524;

Best Local Similarity 100.0%; Pred. No. 5.4e-206;

Matches 524; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 MNLHVWVKLSVSVSLITLYVSHVTLVALSLKHLADCLCDKDYDTLLQTLNGLPINTSH 60

Db 1 MNLVVKKLSVSVLIITYSHVTSKLEHLADCLDKDYDTLLQTLNGLPHINTSH 60
Qy 61 HVVIVGAGMAGLTAAKLLQDAGHTVTILEANDRVGRVETVYRNEKEGYAEMGAMRIPSS 120
Db 61 HVVIVGAGMAGLTAAKLLQDAGHTVTILEANDRVGRVETVYRNEKEGYAEMGAMRIPSS 120
Qy 121 HRIYQWFKVLGVEMNEFVMTDDNTFYLVNGVRERTYVQENPDVLYKNVSESEKGISAD 180
Db 121 HRIYQWFKVLGVEMNEFVMTDDNTFYLVNGVRERTYVQENPDVLYKNVSESEKGISAD 180
Qy 181 DLLDRALQKVEEVEANGCKAALKEKYDRYSVKEVYKKEGGSLSPGAVRMIGDILLNEQSLMY 240
Db 181 DLLDRALQKVEEVEANGCKAALKEKYDRYSVKEVYKKEGGSLSPGAVRMIGDILLNEQSLMY 240
Qy 241 TALSEMIYQADVNDVSVTYHEVTGSDLLPEAFLSVLDPILLNSKVKHIRQSDKGVIVS 300
Db 241 TALSEMIYQADVNDVSVTYHEVTGSDLLPEAFLSVLDPILLNSKVKHIRQSDKGVIVS 300
Qy 301 YOTGNESLMDSADIVLVTTTAKAALFIDFPDPLSISKMEALRSVHYDSSTKILLTFRD 360
Db 301 YOTGNESLMDSADIVLVTTTAKAALFIDFPDPLSISKMEALRSVHYDSSTKILLTFRD 360
Qy 361 KFWEDDGIRGGKSITDGPRIYIYPSHSFHTNETIGVLLASYTWSDESLLFLGASDBELK 420
Db 361 KFWEDDGIRGGKSITDGPRIYIYPSHSFHTNETIGVLLASYTWSDESLLFLGASDBELK 420
Qy 421 ELALRLAKIHGEQWQDKCTGVIIVKWSADPYSLGAFALFTPYQHLEVAQELFSSEGRVH 480
Db 421 ELALRLAKIHGEQWQDKCTGVIIVKWSADPYSLGAFALFTPYQHLEVAQELFSSEGRVH 480
Qy 481 FAGEHTAPPHAWIETSMKSARAATNINKVANESESTIEHTKDEL 524
Db 481 FAGEHTAPPHAWIETSMKSARAATNINKVANESESTIEHTKDEL 524

RESULT 2
AD060382
ID AD060382 standard; protein; 523 AA.
XX
AC AD060382;
XX
DT 15-JUL-2004 (first entry)
XX
DE Mouse L-amino acid oxidase protein SeqID2.
XX
KW L-amino acid oxidase; antibacterial; antibacterial sterilisation;
KW hydrogen peroxide supply component; bacterial infection;
KW sexually transmitted disease; livestock; mastitis; antimicrobial; mouse;
KW murine; enzyme.
XX
OS Mus sp.
XX
JP2004105119-A.
XX
PN 08-APR-2004.
XX
PD 19-SEP-2002; 2002JP-00274082.
XX
PF 19-SEP-2002; 2002JP-00274082.
XX
PR 19-SEP-2002; 2002JP-00274082.
XX
PA (SENT-) SENTAN KAGAKU GIJUTSU INCUBATION CENT KK.
XX
DR WPI; 2004-289536/27.
DR N-PSDB; AD060381.
XX
PT Novel L-amino acid oxidase, useful in preparing antibacterial
PT sterilization composition as hydrogen peroxide supply component which is
PT useful for preventing, treating bacterial infection e.g. mastitis.
XX
PS Claim 2; SEQ ID NO 2; 46pp; Japanese.
XX
CC This invention relates to a novel protein having 27-523 amino acids of L-

CC amino acid oxidase having a fully defined amino acid sequence of 523
CC amino acids as given in the specification and L-amino acid oxidase
CC activity. The invention may be useful for the production of compounds
CC with an antibacterial activity. The invention is useful in preparing an
CC antibacterial sterilisation composition as a hydrogen peroxide supply
CC component. The invention is useful for preventing, treating bacterial
CC infections such as sexually transmitted disease in the breast of
CC livestock, for example mastitis, and provides an antimicrobial effect.
CC The present sequence is that of the mouse L-amino acid oxidase protein of
CC the invention.
XX
SQ Sequence 523 AA;
Query Match 38.8%; Score 1048.5; DB 8; Length 523;
Best Local Similarity 43.5%; Pred. No. 1.9e-74;
Matches 226; Conservative 79; Mismatches 166; Indels 49; Gaps 7;
Qy 27 LSLKEHLADCLDKDYDTLLQTLNGLPHINTSHHVIVGAGMAGLTAAKLLQDAGHTVT 86
Db 25 LALYENLVKFCQDDPYEAFLLIAQNGHTSPLSKRVVVVVGAGMAGLVAAKTLQDAGHEVT 84
Qy 87 ILEANDRVGRVETVYRNEKEGYAEMGAMRIPSSHRIYQWFKVLGVEMNEFVMTDDNTF 146
Db 85 ILEASNHGGRVTVLRNKEGWYELGPMRIPESHKLIHTVYQKLGKLNKFNQVDSNTW 144
Qy 147 YLVNGVRERTYVQENPDVLYKNVSESEKGISADDLLDRALQKVEEVEANGCKAALKEKY 206
Db 145 YLLNGQRYASEVNMANGILGYLPURSEKKNKTVDLFPYQAITKIPHRKTSNCQLLSLY 204
Qy 207 DRYSVKEYLKEEGSLSPGAVRMIGDILLNEQSLMYTALSEMIYQADVNDVSVT--YHEVTG 264
Db 205 DSVSTKAYLMKEGTLSEKAGR-----DDRGYNENAGYKSLLG 243
Qy 265 GSD-----LLPEAFL-----SVLDVPILLNSKVKHIRQSDKGVIVSYQT- 303
Db 244 VSEDCKHLQKCPFRDHRWLCPIPNGLSASLKGPTIRLMSKVRVVRDGPVKVMYRTD 303
Qy 304 GNESLMDSADIVLVTTTAKAALFIDFPDPLSISKMEALRSVHYDSSTKILLTFRQKFW 363
Db 304 GPTSALHKLTAADVAIITASAKATRLITFQPLSREKTHALRSVHYTSATKVVLCVNERFW 363
Qy 364 EDGIRGGKSITDGPRIYIYPSHSFHTNETIGVLLASYTWSDESLLFLGASDBELKELA 423
Db 364 EQDGIRGYSITDRPSRFIYPSHSLPGGK--GVLLASFTVGDDSSFAALKPQVVDVW 421
Qy 424 LRDLAKTH---GEQWQDKCTGVIIVKWSADPYSLGAFALFTPYQHLEVAQELFSSEGRVH 480
Db 422 LDDLAAVHRIPKEELKRMCPKSAIKHWSLDPITIGAFTEFTPYQFVDYSKOLSQPEGRYI 481
Qy 481 FAGEHTAPPHAWIETSMKSARAATNINKVANESESTIEHT 520
Db 482 FAGEHTCLPHSWIDTAIRSGIRASCNIOAAVDEKTRGHT 521
RESULT 3
ABB10103
ID ABB10103 standard; protein; 630 AA.
XX
AC ABB10103;
XX
DT 01-JUL-2002 (first entry)
XX
DE Mouse immediate early interleukin-four induced protein.
XX
KW Interleukin-four induced protein; IL-4; cytostatic; antifungal;
KW antibacterial; immunomodulator; antiinflammatory; dermatological;
KW immunosuppressive; immune disease; tumour; fungal infection;
KW bacterial infection; systemic lupus erythematosus;
KW inflammatory bowel disease; Guillain-Barre syndrome; Whipple's disease;
KW atopic dermatitis; food hypersensitivity; rheumatoid arthritis;
KW osteoarthritis; diabetes mellitus; psoriasis; gene therapy; mouse.
XX
OS Mus sp.

CC translation product does not have the key residues which covalently bind
 CC the FAD cofactor, and so may not exhibit monamine oxidase activity. The
 CC cellular types which express messages encoding YTF03 suggest that signals
 CC important in cell differentiation and development are mediated by them.
 CC The invention provides a process for recombinant production of YTF03,
 CC host cells, expression vectors and specific antibodies. The products can
 CC be used for detection, diagnosis, development of therapeutic methods and
 CC drug screening
 XX
 SQ Sequence 567 AA;

Query Match 37.0%; Score 999; DB 2; Length 567;
 Best Local Similarity 41.8%; Pred. No. 1.8e-70;
 Matches 217; Conservative 99; Mismatches 171; Indels 32; Gaps 9;

QY 3 LHVWVKLSVSVLITLYSHT-VALSLKEHLADCLDCKDYDTLLQTLNDGLPHINTSHH 61
 DB 6 LHL-----LVLPILLSVASQDWKAERSQDPPEKCMQDPDYEQLLKVVVTWGLNRTLPQR 61
 QY 62 VVIVGAGMAGLTAALKLQDAGHTVTILEANDRVGGRVETRYNEKEGVAEMGAMRIPSSH 121
 DB 62 VIVVGAGVAGLVAAKVLSADAGHKVTLLEADNRIGGRIFTYRDQNTGWIGELGAMRMPSSH 121
 QY 122 RIVQWFVKLVGMENFVMTDNTFYLVNGVRERTYVVOENPDVLKYNVSEKIGISADD 181
 DB 122 RIHLKLCQGLGLNLTKFTQYDKNTWTEVHEVKLRNVVEKVPKLGVALRPOEKHSPED 181
 QY 182 LLDRALQKVEEVEANGCKAALEKDYRYSVKEYLKEEGSLSPGAVRMIGDLLNEQSLMYT 241
 DB 182 IYQMALNQALKDLKALGCRKAMKFERHTLLELLEGNSLRPAVQLLDVMSDEGFFYL 241
 QY 242 ALSEMIYDQADVNDSTVYHEVTGSDLLPEAFLSVLDVPIILNSKVKHRSQDKGVIVSY 301
 DB 242 SFAEALRAHSCLSRLQYSRIVGGWDLPLRALSSLSGLVLLNAPVAMTQCPHDVHQI 301
 QY 302 QTGNES-SLMDLSADIVLVTAKAALFDIDPPLISKMEALRSVHVDSSTKILLTPRD 360
 DB 302 ETPSPARNLKVLIKADVLLTASGPAVKRITFSPPLRHMQEARLRLHYVPATKVFLSRR 361
 QY 361 KFEWDDGIRGKSIITDGPRIYIYPSHSPHTNETIGVLLASVTWSDSILLFLGASDELK 420
 DB 362 PFWRREHTEGHSNTDRSRMIFYP-----PPREGALLASTWSDAAAFAAGLSREAL 416
 QY 421 ELALRDLAKIHG---EQWMDKCTGVIVKWSADPYSLGAFALFTPYQHLEYAQELFSSE- 476
 DB 417 RLALDDVAALHGPVVRQLWDG-TGV-VKRWAEQHSQGFVQPP-----ALWQTEK 466
 QY 477 -----GRVHPAGEHTAFPHAWITSMKSAIRAATNIN 508
 DB 467 DDWTVPYGRIFPAGEHTAYPHGWVETAVKSALRAAIAKIN 505

RESULT 5
 ID AAY06480
 XX AAY06480 standard; protein; 567 AA.
 AC AAY06480;
 XX
 DT 27-SEP-1999 (first entry)
 XX
 DE Human tumour-associated protein PRO1265.
 XX
 KW PRO1265; UNQ636; cancer; tumour; diagnosis; therapy; human.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..21
 FT /note= "signal peptide"
 FT Protein 22..567
 FT /note= "mature protein"
 FT Modified-site 54..57
 FT /note= "Asn is N-glycosylated"

FT Region 61..80
 FT /note= "homology to D-amino acid oxidase"
 FT Modified-site 134..137
 FT /note= "Asn is N-glycosylated"
 FT Modified-site 220..223
 FT /note= "Asn is N-glycosylated"
 FT Modified-site 559..562
 FT /note= "Asn is N-glycosylated"
 XX
 PN WO9935170-A2.
 XX
 PD 15-JUL-1999.
 XX
 PF 05-JAN-1999; 99WO-US000106.
 XX
 PR 05-JAN-1998; 98US-0070440P.
 PR 29-APR-1998; 98US-0083500P.
 PR 22-MAY-1998; 98US-0086414P.
 PR 10-JUN-1998; 98US-0088742P.
 PR 10-NOV-1998; 98US-0107783P.
 PR 20-NOV-1998; 98US-0109304P.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Botstein D, Goddard A, Gurney AL, Hillan KJ, Lawrence DA, Roy MA;
 PI Wood WI;
 XX
 DR WPI; 1999-430385/36.
 DR N-PSDB; AAX87257.
 XX
 PT Antibody against proteins expressed in neoplastic cells, useful for tumor
 PT diagnosis and treatment.
 XX
 PS Example 1; Fig 8; 162pp; English.
 XX
 CC This sequence represents human PRO1265 (UNQ636), a 62.9 kDa protein (pI
 CC 8.97) encoded by the novel cDNA clone DNA60764 (see AAX87257).
 CC Amplification of DNA60764 occurs in various lung and colon tumours and
 CC cell lines, suggesting a significant role in tumour formation and growth.
 CC Antagonists (e.g. antibodies) directed to PRO1265 may have use in cancer
 CC therapy. The invention identifies 14 genes (see AAX87254-67) that are
 CC amplified in the genome of tumour cells. Such amplification is expected
 CC to be associated with overexpression of the gene product and to
 CC contribute to tumorigenesis. The encoded proteins (see AAY06477-90) may
 CC be useful targets for the diagnosis and/or treatment (including
 CC prevention) of certain cancers, and may act as predictors of the
 CC prognosis of tumour treatment. Antibodies that bind the proteins are
 CC claimed and used in claimed cancer diagnostic kits
 XX
 SQ Sequence 567 AA;

Query Match 37.0%; Score 999; DB 2; Length 567;
 Best Local Similarity 41.8%; Pred. No. 1.8e-70;
 Matches 217; Conservative 99; Mismatches 171; Indels 32; Gaps 9;

QY 3 LHVWVKLSVSVLITLYSHT-VALSLKEHLADCLDCKDYDTLLQTLNDGLPHINTSHH 61
 DB 6 LHL-----LVLPILLSVASQDWKAERSQDPPEKCMQDPDYEQLLKVVVTWGLNRTLPQR 61
 QY 62 VVIVGAGMAGLTAALKLQDAGHTVTILEANDRVGGRVETRYNEKEGVAEMGAMRIPSSH 121
 DB 62 VIVVGAGVAGLVAAKVLSADAGHKVTLLEADNRIGGRIFTYRDQNTGWIGELGAMRMPSSH 121
 QY 122 RIVQWFVKLVGMENFVMTDNTFYLVNGVRERTYVVOENPDVLKYNVSEKIGISADD 181
 DB 122 RIHLKLCQGLGLNLTKFTQYDKNTWTEVHEVKLRNVVEKVPKLGVALRPOEKHSPED 181
 QY 182 LLDRALQKVEEVEANGCKAALEKDYRYSVKEYLKEEGSLSPGAVRMIGDLLNEQSLMYT 241
 DB 182 IYQMALNQALKDLKALGCRKAMKFERHTLLELLEGNSLRPAVQLLDVMSDEGFFYL 241
 QY 242 ALSEMIYDQADVNDSTVYHEVTGSDLLPEAFLSVLDVPIILNSKVKHRSQDKGVIVSY 301
 DB 242 SFAEALRAHSCLSRLQYSRIVGGWDLPLRALSSLSGLVLLNAPVAMTQCPHDVHQI 301

Db	242	SFAEALRAHSCLSDBLQYSRIVGGWDLLPRALLSSLSGLVLNLPVAVMTQGPDPHVHVOI	301	PR	18-SEP-1998;	98US-0100848P.
Oy	302	QTGNES-SLMDSADIVLTTTAKAALFIDFDPPLSISKMEALRSVHYDSSTKILLTRFD	360	PR	18-SEP-1998;	98US-0100849P.
Db	302	ETSPARNLKVLIKADVLLTASGPAVKRITTFSPPLPRHQEALRLHVVPATKVLSPRR	361	PR	18-SEP-1998;	98US-0101014P.
Oy	361	KPWEDDGRGKSIYDGSRYIYPSHSFHTNETIGVLLASTWDSLSLLFLGASDEBLK	420	PR	18-SEP-1998;	98US-0101068P.
Db	362	PFWREHEGGHSNDRPSRMIFYP-----PPREGALLASTWSDAAAFAGLSREBAL	416	PR	22-SEP-1998;	98US-0101071P.
Oy	421	ELALRDLAKING--EQWMDKCTGIVVKWSADPYSLGAFAFLFTPYQHLEVAQELFSSE-	476	PR	23-SEP-1998;	98US-0101279P.
Db	417	RLALDDVAALHGPPVRQWLDG-TGV-VKRWEDQHSQGFVVQPP-----ALWQTEK	466	PR	23-SEP-1998;	98US-0101471P.
Oy	477	-----GRVHFAQSHTAPPAHWIETSMKSAIRAATNIN 508		PR	23-SEP-1998;	98US-0101472P.
Db	467	DDWTPVYGRIFYAGEHTAYPHGWVETAVKSALRAAIKIN 505		PR	23-SEP-1998;	98US-0101473P.
RESULT 6				PR	23-SEP-1998;	98US-0101475P.
AAV99364				PR	23-SEP-1998;	98US-0101476P.
ID	AAV99364	standard; protein; 567 AA.		PR	23-SEP-1998;	98US-0101477P.
XX	AAV99364;			PR	24-SEP-1998;	98US-0101738P.
DT	08-AUG-2000 (first entry)			PR	24-SEP-1998;	98US-0101741P.
DE	Human PRO1265 (UNQ636) amino acid sequence SEQ ID NO:84.			PR	24-SEP-1998;	98US-0101743P.
XX	Human; PRO polypeptide; membrane bound protein; receptor; diagnosis;			PR	24-SEP-1998;	98US-0101915P.
KW	transmembrane; secretion; immunoadhesion; pharmaceutical; screening.			PR	24-SEP-1998;	98US-0101916P.
XX	Homo sapiens.			PR	29-SEP-1998;	98US-0102207P.
XX	WO200012708-A2.			PR	29-SEP-1998;	98US-0102240P.
PN	09-MAR-2000.			PR	29-SEP-1998;	98US-0102307P.
PD	01-SEP-1999; 99WO-US020111.			PR	29-SEP-1998;	98US-0102330P.
PF	01-SEP-1998; 98US-0098716P.			PR	29-SEP-1998;	98US-0102331P.
XX	01-SEP-1998; 98US-0098749P.			PR	30-SEP-1998;	98US-0102484P.
PR	02-SEP-1998; 98US-0098803P.			PR	30-SEP-1998;	98US-0102570P.
PR	02-SEP-1998; 98US-0098821P.			PR	30-SEP-1998;	98US-0102571P.
PR	02-SEP-1998; 98US-0098843P.			PR	01-OCT-1998;	98US-0102684P.
PR	09-SEP-1998; 98US-0099538P.			PR	01-OCT-1998;	98US-0102687P.
PR	09-SEP-1998; 98US-0099596P.			PR	02-OCT-1998;	98US-0102965P.
PR	09-SEP-1998; 98US-0099602P.			PR	06-OCT-1998;	98US-0103258P.
PR	09-SEP-1998; 98US-0099642P.			PR	06-OCT-1998;	98US-0103449P.
PR	10-SEP-1998; 98US-0099741P.			PR	07-OCT-1998;	98US-0103314P.
PR	10-SEP-1998; 98US-0099754P.			PR	07-OCT-1998;	98US-0103315P.
PR	10-SEP-1998; 98US-0099763P.			PR	07-OCT-1998;	98US-0103328P.
PR	10-SEP-1998; 98US-0099792P.			PR	07-OCT-1998;	98US-0103395P.
PR	10-SEP-1998; 98US-0099808P.			PR	07-OCT-1998;	98US-0103401P.
PR	10-SEP-1998; 98US-0099813P.			PR	08-OCT-1998;	98US-0103633P.
PR	10-SEP-1998; 98US-0099815P.			PR	08-OCT-1998;	98US-0103678P.
PR	10-SEP-1998; 98US-0099818P.			PR	08-OCT-1998;	98US-0103679P.
PR	15-SEP-1998; 98US-0100385P.			PR	08-OCT-1998;	98US-0103711P.
PR	15-SEP-1998; 98US-0100388P.			PR	14-OCT-1998;	98US-0104257P.
PR	15-SEP-1998; 98US-0100390P.			PR	20-OCT-1998;	98US-0104987P.
PR	16-SEP-1998; 98US-0100584P.			PR	20-OCT-1998;	98US-0105000P.
PR	16-SEP-1998; 98US-0100627P.			PR	20-OCT-1998;	98US-0105002P.
PR	16-SEP-1998; 98US-0100661P.			PR	21-OCT-1998;	98US-0105104P.
PR	16-SEP-1998; 98US-0100662P.			PR	22-OCT-1998;	98US-0105169P.
PR	16-SEP-1998; 98US-0100664P.			PR	22-OCT-1998;	98US-0105266P.
PR	17-SEP-1998; 98US-0100683P.			PR	26-OCT-1998;	98US-0105693P.
PR	17-SEP-1998; 98US-0100684P.			PR	26-OCT-1998;	98US-0105694P.
PR	17-SEP-1998; 98US-0100710P.			PR	27-OCT-1998;	98US-0105807P.
PR	17-SEP-1998; 98US-0100711P.			PR	27-OCT-1998;	98US-0105881P.
PR	17-SEP-1998; 98US-0100919P.			PR	27-OCT-1998;	98US-0105882P.
PR	17-SEP-1998; 98US-0100930P.			PR	27-OCT-1998;	98US-0106062P.
PR				PR	28-OCT-1998;	98US-0106023P.
PR				PR	28-OCT-1998;	98US-0106030P.
PR				PR	28-OCT-1998;	98US-0106032P.
PR				PR	28-OCT-1998;	98US-0106033P.
PR				PR	28-OCT-1998;	98US-0106178P.
PR				PR	29-OCT-1998;	98US-0106248P.
PR				PR	29-OCT-1998;	98US-0106384P.
PR				PR	29-OCT-1998;	98US-0108500P.
PR				PR	30-OCT-1998;	98US-0106464P.
PR				PR	03-NOV-1998;	98US-0106856P.
PR				PR	03-NOV-1998;	98US-0106902P.
PR				PR	03-NOV-1998;	98US-0106905P.
PR				PR	03-NOV-1998;	98US-0106919P.
PR				PR	03-NOV-1998;	98US-0106932P.
PR				PR	03-NOV-1998;	98US-0106934P.
PR				PR	10-NOV-1998;	98US-0107783P.
PR				PR	17-NOV-1998;	98US-0108775P.

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PR 17-NOV-1998; 98US-0108779P.
PR 17-NOV-1998; 98US-0108787P.
PR 17-NOV-1998; 98US-0108788P.
PR 17-NOV-1998; 98US-0108801P.
PR 17-NOV-1998; 98US-0108802P.
PR 17-NOV-1998; 98US-0108806P.
PR 17-NOV-1998; 98US-0108807P.
PR 17-NOV-1998; 98US-0108867P.
PR 17-NOV-1998; 98US-0108925P.
PR 18-NOV-1998; 98US-0108848P.
PR 18-NOV-1998; 98US-0108849P.
PR 18-NOV-1998; 98US-0108850P.
PR 18-NOV-1998; 98US-0108851P.
PR 18-NOV-1998; 98US-0108852P.
PR 18-NOV-1998; 98US-0108858P.
PR 18-NOV-1998; 98US-0108904P.
XX (GETH ) GENENTECH INC.
XX
XX Baker K, Goddard A, Gurney AL, Smith V, Watanabe CK, Wood WI;
XX
XX WPI: 2000-237871/20.
XX N-PSDB; AAA37046.
XX
XX New mammalian DNA sequences encoding transmembrane, receptor or secreted
XX PRO polypeptides, useful for screening of potential peptide or small
XX molecule inhibitors of the relevant receptor/ligand interactions.
XX
XX Claim 12; Fig 50; 773pp; English.
XX
XX AAA37022 to AAA37144 encode the new isolated human transmembrane,
XX receptor or secreted PRO polypeptides given in AAY99340 to AAY99462. The
XX transmembrane and receptor PRO proteins can be used for screening of
XX potential peptide or small molecule inhibitors of the relevant
XX receptor/ligand interactions. The polypeptides and nucleotide sequences
XX encoding them have various industrial applications, including uses as
XX pharmaceutical and diagnostic agents. AAA37145 to AAA37330 represent PCR
XX primers and hybridisation probes used in the isolation of the PRO
XX polypeptides from the present invention
XX
XX Sequence 567 AA;
XX
XX Query Match 37.0%; Score 999; DB 3; Length 567;
XX Best Local Similarity 41.8%; Pred. No. 1.8e-70;
XX Matches 217; Conservative 99; Mismatches 171; Indels 32; Gaps 9;
XX
QY 3 LHVVKWKLVSQVSLTLYYSHT-VALSKEHADIADLEKDYDTLLQTLNDGLPHINTSHH 61
DB 6 LHL-----LVLPILLSVASQDWKAERSQDPPEKCMQDPDYEQLLKVVVTWGLNRTLKPQR 61
QY 62 VVIVGAGMAGLTAALLQDAGHTVTILEANDRVGGRVETRYNEKEGWAEMCAMRIPSSH 121
DB 62 VVIVGAGVAGLVAAKVLSDAGHKVTLISADNRIGRIFTYRDQNTGWIGELGAMRMPSSH 121
QY 122 RIVQVFKVLGVEMNEFEVMTDNTFYLNGVRERTYVQENPDVLKYNVSESEKISADD 181
DB 122 RLHLKLCQGLGLNLTKFYQDKNTVEHVVKLVYVVEKVPKLGVALRPOEKGHSPED 181
QY 182 LLDRALQKVEVEANGKAALEKYDYSVKEYLKEEGLSPGAVRMI GDLNLEOSLMYT 241
DB 182 IYQMALNQALKOLKALGCRKAMKPFERTLTLEYLLGEGNLSRPAVQLLGDVMSDEGFFYL 241
QY 242 ALSEMIYQADNVSVTHVETVGGSDLLPEAFSLVDVPIILNSKVKHQRQSKGVIVSY 301
DB 242 SFAEALRAHSCUSDLRLQSRIVGGWDLPLRALLSGLVLLNAPVAVMTQGHVHVQI 301
QY 302 QTGNES-SIMDLASDIVLVTITAKAALFTIDPPLISIKMEALRSVHYDSSSTKILLTPRD 360
DB 302 ETSPPARNLKVLLKADVLLTAGSPAVKRTFSPPLPRHQEALRLHYVPATKVPFLSFR 361
QY 361 KPWEDDGIRGKSIITDGSRIYIYPSHFNHNETIGVLLASVTWSDLSLLFLGASDEELK 420
DB 362 PFWREHIEGGHNSNDRPSRMIFYP-----PPREGALLASVTWSDAAAFAGLSREAL 416
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QY 421 ELALRDLAKIHG---EOWWDKCTGVIVKKGADPVSLGAFALFTPYQHLEVAQELFSSE- 476
DB 417 RLALDDVAALHGPPVRQLWDG-TGV-VKRWEDQHSQSGFVVQPP-----ALWQTEK 466
QY 477 -----GRVHFACEHTAFPHAWIETSMKSAIRAATNIN 508
DB 467 DDWTVVPYGRIFYFACEHTAYPHGWVETAVKSALRAAIKIN 505

RESULT 7
AAY93687
ID AAY93687 standard; protein; 567 AA.
XX
AC AAY93687;
XX
DT 03-OCT-2000 (first entry)
XX
DE Amino acid sequence of novel polypeptide PRO1265.
XX
KW PRO201; PRO292; PRO327; PRO1265; PRO344; PRO347; PRO357; PRO715;
KW PRO1017; PRO1112; PRO509; PRO853; PRO882; tumour cell; tumourigenesis;
KW cancer; neoplastic cell growth; cell proliferation.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..21
FT Modified-site /note= "signal peptide"
FT Modified-site 35..43
FT Modified-site /note= "Tyrosine kinase phosphorylation site"
FT Domain /note= "N-glycosylation site"
FT Region /note= "transmembrane domain"
FT Modified-site 59..75
FT Modified-site /note= "D-amino oxidases proteins site"
FT Modified-site 134..138
FT Modified-site /note= "N-glycosylation site"
FT Modified-site 161..169
FT Modified-site /note= "Tyrosine kinase phosphorylation site"
FT Modified-site 220..224
FT Modified-site /note= "N-glycosylation site"
FT Modified-site 559..563
FT Modified-site /note= "N-glycosylation site"
XX
XX WO200037640-A2.
XX
XX 29-JUN-2000.
XX
XX 16-DEC-1999; 99WO-US030095.
XX
XX 22-DEC-1998; 98US-0113296P.
XX 08-MAR-1999; 99WO-US005028.
XX 02-JUN-1999; 99WO-US012252.
XX 01-SEP-1999; 99WO-US020111.
XX 15-SEP-1999; 99WO-US021090.
XX 30-NOV-1999; 99WO-US028313.
XX 01-DEC-1999; 99WO-US028409.
XX 02-DEC-1999; 99WO-US028301.
XX 02-DEC-1999; 99WO-US028565.
XX (GETH ) GENENTECH INC.
XX
XX Botstein D, Goddard A, Gurney AL, Hillan K, Lawrence DA, Roy MA;
XX Wood WI;
XX
XX WPI: 2000-452188/39.
XX N-PSDB; AAA46906.
XX
XX New anti-polypeptide antibody useful in the treatment and diagnosis of
XX neoplastic cell growth and proliferation.
XX
```

PS Claim 61; Fig 8; 220pp; English.

XX The present sequence represents a novel human polypeptide. The

CC specification describes novel polypeptides designated PRO201, PRO292,

CC PRO327, PRO1265, PRO344, PRO347, PRO357, PRO715, PRO1017, the

CC PRO1112, PRO509, PRO853 and PRO882. These genes are amplified in the

CC genome of tumour cells. The polypeptides are believed to contribute to

CC tumourigenesis. The polypeptides are useful target for the identification

CC of certain cancers, and may act as predictors of the prognosis of tumour

CC treatment. Antibodies against these polypeptides are useful in the

CC treatment and diagnosis of neoplastic cell growth and proliferation in

CC mammals

XX Sequence 567 AA;

SQ

Query Match 37.0%; Score 999; DB 3; Length 567;

Best Local Similarity 41.8%; Pred. No. 1.8e-70;

Matches 217; Conservative 99; Mismatches 171; Indels 32; Gaps 9;

QY 3 LHVVKWKLVSIVLITLYSHT-VALSLKEHLADCLDKDYDTLLQTLDNLGPHINTSHH 61

DB 6 LHL-----LVLVPIILLSVASQDWAERSQDPFEKCMQDPDYEQLLKVVTVGLNRLTKPQR 61

QY 62 VVIVGAGAGLTAAGLQDAGHTVILEANDRVGRVETRYNEKEGVAEMGAMRIPSSH 121

DB 62 VVIVGAGAGLVAAGVLSAGHKVTLLEADNRIGRIFTYRDQNTGWIGELGAMRMPSSH 121

QY 122 RIVQWFKVKGVEEMNEFMTDNTFYLVNGVRETYVVOENPDVLKYNVSEKGISADD 181

DB 122 RILHLKCOGLNLTKFTQYDKNTWTEVHEVKLRNVVVEKVPKLGVALRPOKGHSPED 181

QY 182 LLDRLALQVKVEANGKAALEKYDRYSVKEYLKEEGLSPCAVRMTGDLNLSQSLMYT 241

DB 182 IQVMALNQALKDLKALGCKEAMKFERHTLLEYLLGEGNLSRPAVQLLDGVMSEGGFFYL 241

QY 242 ALSEMIYDQADVNDVSVTHVETGSDLLPEAFSLVDVPIILNSKVKHROSQDKGIVSY 301

DB 242 SFAEALRAHSCLSDRLOYSRIVGGWDLPLRALSSLSGLVLNAPVAVMTQCPHDVHVOI 301

QY 302 QTGNES-SLMDLSADIVLTTTAKAALFIDPDPPLSISKMBALRSVHYDSSTKILLTPRD 360

DB 302 ETSPPARNLKVLAQVLLTASGPAVKRITPSPPLPRHMQEALRLHVVPAVKVFLSPFR 361

QY 361 KFWEDDGIKGGKSIITDGPISYIYPSHSFHTNETIGVLLASVTWSDSLLFLGASDEBLK 420

DB 362 PWREHEHGGHSNTDRPSRMIFYP-----PPREGALLASVTWSDAATAAAGLSREBAL 416

QY 421 ELALRDLAKIHG---EQWMDKCTGIVVKWSADPYSLGAFALFTPYQHLEYAQELFSSE- 476

DB 417 RLALDDVAALHGPVVRQLWDG-TGV-VKRWEDQHSQGVVQVP-----ALWQTEK 466

QY 477 -----GRVHPAGEHTAPPHAWITSMKSAIRAATNIN 508

DB 467 DDWTVPYGRIYPAGEHTAYPHGWETAVKSAIRAAIKIN 505

RESULT 8

ID AAB66113

XX AAB66113 standard; protein; 567 AA.

XX AAB66113;

AC AAB66113;

XX

DT 02-APR-2001 (first entry)

XX

DE Protein of the invention #25.

XX

KW Secreted; transmembrane; gene therapy.

XX

OS Unidentified.

XX

PN WO200078961-A1.

XX

PD 28-DEC-2000.

XX 18-FEB-2000; 2000WO-US004342.

XX 23-JUN-1999; 99US-0141037P.

PR 20-JUL-1999; 99US-0144758P.

PR 26-JUL-1999; 99US-0145698P.

PR 01-SEP-1999; 99WO-US020111.

PR 29-OCT-1999; 99US-0162506P.

PR 30-NOV-1999; 99WO-US028313.

PR 02-DEC-1999; 99WO-US028551.

PR 16-DEC-1999; 99WO-US030095.

PR 05-JAN-2000; 2000WO-US000219.

PR 06-JAN-2000; 2000WO-US000376.

XX (GETH) GENENTECH INC.

XX Baker KP, Botstein D, Deenoyers L, Eaton DL, Ferrara N, Fong S,

PI Gao W, Goddard A, Godowski FJ, Grimaldi CJ, Gurney AL, Hillan KJ;

PI Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;

PI Williams PM, Wood WI;

XX WPI; 2001-071395/08.

XX

PT Secreted and transmembrane proteins and nucleic acids designated PRO,

PT useful as hybridization probes, in chromosome and gene mapping and gene

PT therapy.

XX

PS Claim 1; Fig 50; 787pp; English.

XX

CC The present invention relates to secreted and transmembrane proteins.

CC These proteins and the DNA encoding them may be used as hybridization

CC probes, in chromosome and gene mapping and in the generation of anti-

CC sense RNA and DNA. They may also be used to generate either

CC transgenic animals or knockout animals which are in turn useful for

CC development and screening of therapeutically useful reagents. The nucleic

CC acids may also be used in gene therapy

XX

SQ Sequence 567 AA;

Query Match 37.0%; Score 999; DB 4; Length 567;

Best Local Similarity 41.8%; Pred. No. 1.8e-70;

Matches 217; Conservative 99; Mismatches 171; Indels 32; Gaps 9;

QY 3 LHVVKWKLVSIVLITLYSHT-VALSLKEHLADCLDKDYDTLLQTLDNLGPHINTSHH 61

DB 6 LHL-----LVLVPIILLSVASQDWAERSQDPFEKCMQDPDYEQLLKVVTVGLNRLTKPQR 61

QY 62 VVIVGAGAGLTAAGLQDAGHTVILEANDRVGRVETRYNEKEGVAEMGAMRIPSSH 121

DB 62 VVIVGAGAGLVAAGVLSAGHKVTLLEADNRIGRIFTYRDQNTGWIGELGAMRMPSSH 121

QY 122 RIVQWFKVKGVEEMNEFMTDNTFYLVNGVRETYVVOENPDVLKYNVSEKGISADD 181

DB 122 RILHLKCOGLNLTKFTQYDKNTWTEVHEVKLRNVVVEKVPKLGVALRPOKGHSPED 181

QY 182 LLDRLALQVKVEANGKAALEKYDRYSVKEYLKEEGLSPCAVRMTGDLNLSQSLMYT 241

DB 182 IQVMALNQALKDLKALGCKEAMKFERHTLLEYLLGEGNLSRPAVQLLDGVMSEGGFFYL 241

QY 242 ALSEMIYDQADVNDVSVTHVETGSDLLPEAFSLVDVPIILNSKVKHROSQDKGIVSY 301

DB 242 SFAEALRAHSCLSDRLOYSRIVGGWDLPLRALSSLSGLVLNAPVAVMTQCPHDVHVOI 301

QY 302 QTGNES-SLMDLSADIVLTTTAKAALFIDPDPPLSISKMBALRSVHYDSSTKILLTPRD 360

DB 302 ETSPPARNLKVLAQVLLTASGPAVKRITPSPPLPRHMQEALRLHVVPAVKVFLSPFR 361

QY 361 KFWEDDGIKGGKSIITDGPISYIYPSHSFHTNETIGVLLASVTWSDSLLFLGASDEBLK 420

DB 362 PWREHEHGGHSNTDRPSRMIFYP-----PPREGALLASVTWSDAATAAAGLSREBAL 416

QY 421 ELALRDLAKIHG---EQWMDKCTGIVVKWSADPYSLGAFALFTPYQHLEYAQELFSSE- 476

DB 417 RLALDDVAALHGPVVRQLWDG-TGV-VKRWEDQHSQGVVQVP-----ALWQTEK 466

QY 477 -----GRVHPAGEHTAPPHAWITSMKSAIRAATNIN 508

DB 467 DDWTVPYGRIYPAGEHTAYPHGWETAVKSAIRAAIKIN 505

Db 242 SFAEALRAHSCLSDRLOYSRIVGGWDLPLRALSSLSGLVLLNAPVAMTQGHVDHVQI 301
Qy 302 QTGNES-SLMDLSADIVLVTAKAALFIDFDPPLSISKWEALRSVHYDSSTKILLTPRD 360
Db 302 ETSPPARNLKVLKADVLLTAGSPAVKRITFPPLPRHQEALRLHYVPATKVLFSFR 361
Qy 361 KFWEDDGIRGKSIITDGPRIYIYPSHSPHTNETIGVLLASYTWSDESLLFLGASDEELK 420
Db 362 PFWEHEHIEGHSNTDRPSRMIFYP-----PPREGALLLASVTWSDAAAFAAGLSREAL 416
Qy 421 ELALRDLAKIHG---EQWMDKCTGVIVKWSADPYSLGAFALFTPYQHLEYAQELFSSE- 476
Db 417 RLALDDVAALHGPVVRQLWDG-TGV-VKRWAEQHSQGGFVVQPP-----ALWQTEK 466
Qy 477 -----GRVHFAGETHAPPHAWIETSMKSIRAATNIN 508
Db 467 DDWTPVPGRIYFAGEHTAYPHGWVETAVKSALRAAIKIN 505

RESULT 10
AAB50962
ID AAB50962 standard; protein; 567 AA.
XX
AC AAB50962;
DT 21-MAR-2001 (first entry)
XX
DE Human PRO1265 protein.
XX
KW Human; PRO; cytostatic; nootropic; neuroprotective; respiratory general;
KW antiinflammatory; antiangiogenic; immunosuppressive; immunostimulant;
KW PRO agonist; cancer; inflammatory disorder; immunological disorder.
XX
OS Homo sapiens.
XX
PN WO200073348-A2.
XX
PD 07-DEC-2000.
XX
PF 30-MAY-2000; 2000WO-US014941.
XX
PR 02-JUN-1999; 99WO-US012252.
PR 22-JUN-1999; 99US-0140650P.
PR 23-JUN-1999; 99US-0141037P.
PR 20-JUL-1999; 99US-0144758P.
PR 01-SEP-1999; 99WO-US020111.
PR 08-SEP-1999; 99WO-US020594.
PR 29-OCT-1999; 99US-0162506P.
PR 30-NOV-1999; 99WO-US028313.
PR 01-DEC-1999; 99WO-US028634.
PR 02-DEC-1999; 99WO-US028551.
PR 09-DEC-1999; 99US-0170262P.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030999.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004342.
PR 02-MAR-2000; 2000WO-US005841.
PR 03-MAR-2000; 2000US-0187202P.
PR 10-MAR-2000; 2000WO-US006319.
PR 15-MAR-2000; 2000WO-US006884.
PR 30-MAR-2000; 2000WO-US008439.
PR 17-MAY-2000; 2000WO-US013705.
XX
(GETH) GENENTECH INC.

XX
XX Baker KP, Goddard A, Gurney AL, Hebert C, Henzel W, Kabakoff RC;
PI Shelton DL, Smith V, Watanabe CK, Wood WI;
XX
DR WPI; 2001-016509/02.
DR N-PSDB; AAC91564.

XX
PT Twenty eight nucleic acids encoding PRO/polypeptides which are useful for
PT treating various tumors, e.g. breast cancer, and other inflammatory,
XX angiogenic and immunological disorders.
PS Claim 31; Fig 24; 188pp; English.
XX
CC The present sequence is one of twenty eight novel PRO polypeptides. The
CC PRO polypeptides and their agonists, including antibodies, peptides, and
CC small molecule agonists, may be used to treat various tumors, e.g.,
CC cancers such as breast cancer, ovarian cancer, renal cancer, colorectal
CC cancer, uterine cancer, prostate cancer, lung cancer, bladder cancer,
CC central nervous system cancer, melanoma or leukaemia. They are also
CC useful for treating other disorders such as neuronal, glial, astrocytal,
CC hypothalamic and other glandular, macrophagal, epithelial, stromal and
CC blastocoealic disorders, and inflammatory, angiogenic and immunological
XX disorders
XX
SQ Sequence 567 AA;

Query Match 37.0%; Score 999; DB 4; Length 567;
Best Local Similarity 41.8%; Pred. No. 1.8e-70;
Matches 217; Conservative 99; Mismatches 171; Indels 32; Gaps 9;
Qy 3 LHVVKWKLVSVLITLYSHT-VALSLKEHLADCLCDKDYDTLLQTLNDGLPHINTSHH 61
Db 6 LHL-----LVLPILLSVASQDWKAERSQDPPEKCMQDPDYBQLLKVVWGLNRLTKPOR 61
Qy 62 VVIVGAGMAGLTAAKLLQDAGHTVITILEANDRVGVRVETRYNEKEGVAEMGAMRIPSSH 121
Db 62 VVIVGAGVAGLVAALKVLSAGHKVITILEADNRIGRIFTYRDQNTGWIGELGAMRMPSSH 121
Qy 122 RIVQWFKVLGVNMFVMTDNTETVLVNGVRRTYVVOENPDVLKYNVSESEKGISADD 181
Db 122 RILHKLCOGLGULNLTFTQYDKNTWTEVHEVKLRNVYVEKPEKLGALURPOEKHSPED 181
Qy 182 LLDRLAQKBEVEANGCKAALEKYDRYSVKEYLKEEGSLSPGAVRMIGDLLNEQSLMYT 241
Db 182 IYQWALNQAALKDLKALGCRKAMKFERHTLLEYLLGEGNLSRPAVQLLGDVMSDGFYFL 241
Qy 242 ALSEMIYDQADVNSVTYHEVTGSDLLPEAFSLVDLPILLNSKVKHIRQSDKGIVISY 301
Db 242 SFAEALRAHSCLSDRLOYSRIVGGWDLPLRALSSLSGLVLLNAPVAMTQGHVDHVQI 301
Qy 302 QTGNES-SLMDLSADIVLVTAKAALFIDFDPPLSISKWEALRSVHYDSSTKILLTPRD 360
Db 302 ETSPPARNLKVLKADVLLTAGSPAVKRITFPPLPRHQEALRLHYVPATKVLFSFR 361
Qy 361 KFWEDDGIRGKSIITDGPRIYIYPSHSPHTNETIGVLLASYTWSDESLLFLGASDEELK 420
Db 362 PFWEHEHIEGHSNTDRPSRMIFYP-----PPREGALLLASVTWSDAAAFAAGLSREAL 416
Qy 421 ELALRDLAKIHG---EQWMDKCTGVIVKWSADPYSLGAFALFTPYQHLEYAQELFSSE- 476
Db 417 RLALDDVAALHGPVVRQLWDG-TGV-VKRWAEQHSQGGFVVQPP-----ALWQTEK 466
Qy 477 -----GRVHFAGETHAPPHAWIETSMKSIRAATNIN 508
Db 467 DDWTPVPGRIYFAGEHTAYPHGWVETAVKSALRAAIKIN 505

RESULT 11
AAU12409
ID AAU12409 standard; protein; 567 AA.
XX
AC AAU12409;
XX
XX 24-OCT-2001 (first entry)
XX
XX Human PRO1265 polypeptide sequence.
XX
KW Human secretory and transmembrane; PRO; mammalian; cancer; lung; breast;
KW prostate; cervical; tumour necrosis factor-alpha; TNF-alpha; cartilage;

KW rheumatoid arthritis; myocardial infarction; thrombophlebitis;
 KW lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma;
 KW wound healing; chromosome mapping; gene mapping.

OS Homo sapiens.

PN WO200200690-A2.

XX 03-JAN-2002.

XX 20-JUN-2001; 2001WO-US019692.

XX 23-JUN-2000; 2000US-02113637P.

XX 20-JUL-2000; 2000US-0219556P.

XX 25-JUL-2000; 2000US-0220624P.

XX 25-JUL-2000; 2000US-0220664P.

XX 28-JUL-2000; 2000WO-US020710.

XX 02-AUG-2000; 2000US-0222695P.

XX 17-AUG-2000; 2000US-00641657.

XX 23-AUG-2000; 2000WO-US023522.

XX 24-AUG-2000; 2000WO-US023328.

XX 07-SEP-2000; 2000US-0230978P.

XX 18-SEP-2000; 2000US-00664610.

XX 18-SEP-2000; 2000US-00665350.

XX 24-OCT-2000; 2000US-0242922P.

XX 08-NOV-2000; 2000US-00709238.

XX 08-NOV-2000; 2000WO-US030952.

XX 01-NOV-2000; 2000WO-US030873.

XX 01-DEC-2000; 2000WO-US032678.

XX 20-DEC-2000; 2000US-00747259.

XX 20-DEC-2000; 2000WO-US034956.

XX 22-JAN-2001; 2001US-00802706.

XX 14-MAR-2001; 2001US-00806889.

XX 22-MAR-2001; 2001US-00816744.

XX 28-FEB-2001; 2001US-00796498.

XX 28-FEB-2001; 2001WO-US006520.

XX 01-MAR-2001; 2001WO-US006666.

XX 09-MAR-2001; 2001US-00802706.

XX 14-MAR-2001; 2001US-00806889.

XX 22-MAR-2001; 2001US-00816744.

XX 05-APR-2001; 2001US-00828366.

XX 10-MAY-2001; 2001US-00854208.

XX 10-MAY-2001; 2001US-00854280.

XX 25-MAY-2001; 2001US-00866028.

XX 25-MAY-2001; 2001US-00866034.

XX 25-MAY-2001; 2001WO-US017092.

XX 30-MAY-2001; 2001US-00870574.

XX 01-JUN-2001; 2001WO-US017443.

XX 01-JUN-2001; 2001WO-US017800.

PA (GETH) GENENTECH INC.

PI Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;

PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;

PI Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;

XX WPI; 2002-090516/12.

XX N-PSDB; ABL88159.

XX One hundred and eighty seven nucleic acids encoding PRO polypeptides,

XX useful in diagnosis and treatment of cardiovascular (e.g. myocardial

XX infarction), endothelial or angiogenic disorders in a mammal.

XX Claim 11; Fig 176; 565pp; English.

XX ABL88072 to ABL88258 encodes the PRO proteins given in ABL884817 to
 CC ABL885003. The PRO proteins and polynucleotides have cardiant, cytostatic,
 CC antiangiogenic, hypotensive, vulnary and antiarteriosclerotic
 CC activities, and can be used in gene therapy. The PRO polynucleotides,
 CC proteins, agonists and antagonists are useful for treating or diagnosing
 CC a cardiovascular, endothelial or angiogenic disorder in a mammal, e.g.
 CC cardiac hypertrophy, trauma, cancer, age-related macular degeneration,
 CC atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis,
 CC angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour
 CC angiogenesis (such as breast carcinoma and liver carcinoma) and wound

CC healing. The PRO polynucleotides have applications in molecular biology,
 CC including use as hybridisation probes, and in chromosome and gene
 CC mapping. ABL88259 to ABL88267 represent primers and probes used in the
 CC exemplification of the present invention

XX SQ Sequence 567 AA;

Query Match 37.0%; Score 999; DB 5; Length 567;

Best Local Similarity 41.8%; Pred. No. 1.8e-70;

Matches 217; Conservative 99; Mismatches 170; Indels 32; Gaps 9;

QY 3 LHVVKWKLVSIVLITLYSHT-VALSLKEHLADLCEDKDYDTLLQTLDNGLPHINTSHH 61

DB 6 LHL-----LVLPILLSVASQDWKAERSQDPFEKCMQDPDYBQLLVVWVWGLNRTLKPOR 61

QY 62 VVIVGAGMAGLTAAKLLQDAGHTVILEANDRVGRVETRYNEKEGWAEMGAMRIPSSH 121

DB 62 VVIVGAGVAGLVAAKVLSDAGHKVILEADNRIGRIFTYRDQNTGWGELGAMRMPSSH 121

QY 122 RIVQWFKVLGVEMNEFVMTDNTFYLNVGRERTYVVOENPDVLKYNVSESEKGISADD 181

DB 122 RILHKLCOGLNLTKFTQYDKNTWTEVHEVKLRNVVVEKVPKLGALRPOEKGHSPED 181

QY 182 LLDRALOKVEVEANGCKAALEKVDYSVREYLYKEEGLSPCAVRMIGDLLNEQSLMYT 241

DB 182 IYQMALNQALKDKALGCRKAMKPFERHTLLEYLLGEGNLSRPAVQLLDVMSDGFYFL 241

QY 242 ALSEMIYDQADVNDSTVYHEVTGGDLPEAFSLVDVPIILLNSKVKHQRSDKGVISY 301

DB 242 SFAELRAHSCLSRLQYSRIVGGWDLPLRALLSLSGLVLLNAPVAMTQPHDVHVOI 301

QY 302 QTGNES-SLMDLSADIVLVTTTAKAALFIDPPPLSISKMEALRSVHYDSSTKILLTFRD 360

DB 302 ETSPPARNLKVLEKADVLLTASGPAVKRIITSPPLPRHQEALRLHVVYPATKVFLSFPR 361

QY 361 KFWEDDGIRGKSTIDGSRVYIYPPSHSFHNTETIGVLLASYSDESLLFLGASDEELK 420

DB 362 PFWEHEIEGHGHSNTDRSRMIFYP-----PPREGALLASYTWSDAFAAGLSREAL 416

QY 421 ELALDLAKIHG---EQWMDCTGVIVKKAADPYSLGAFALFTPYQHLEVAQELFSSE- 476

DB 417 RLALDDVAALHGPVVRQLWDG-TGV-VKRWEDQHSQGGFVVQPP-----ALWQTEK 466

QY 477 -----GRVHAGEHTAFPHAMTSMKSAIRAATNIN 508

DB 467 DDWTPVYGRIVYAGEHTAYPHGWETAVKSAALRAAIKIN 505

RESULT 13

ABB10104

ID ABB10104 standard; protein; 567 AA.

XX AC ABB10104;

XX DT 01-JUL-2002 (first entry)

XX DE Human immediate early interleukin-four induced protein.

XX KW Interleukin-four induced protein; IL-4; cytostatic; antifungal;

XX KW antibacterial; immunomodulator; antiinflammatory; dermatological;

XX KW immunosuppressive; immune disease; tumour; fungal infection;

XX KW bacterial infection; systemic lupus erythematosus;

XX KW inflammatory bowel disease; Guillain-Barre syndrome;

XX KW atopic dermatitis; food hypersensitivity; rheumatoid arthritis;

XX KW osteoarthritis; diabetes mellitus; psoriasis; gene therapy; human.

XX OS Homo sapiens.

XX XX WO200218574-A2.

XX PN 07-MAR-2002.

XX PD 24-AUG-2001; 2001WO-US026462.

XX PF

XX PR 25-AUG-2000; 2000US-0227818P.
XX PA (NSHO-) NORTH SHORE-LONG ISLAND JEWISH RES.
XX PI Chu CC, Chavan SS, Mason JM;
XX DR WPI; 2002-329772/36.
XX PT New human immediate early interleukin-four (IL-4) induced protein and
PT polynucleotides, useful for preventing or treating immune related
PT disease, tumor, fungal or bacterial infection, e.g. lupus erythematosus
PT or Whipple's disease.
XX PS Claim 1(a); Page 5; 61pp; English.
XX CC The invention relates to an isolated polynucleotide, which encodes a
CC human immediate early interleukin-four (IL-4) induced protein. The
CC activity of the polynucleotide of the invention may be described as,
CC cytostatic, antifungal, antibacterial, immunomodulator, antiinflammatory,
CC dermatological and immunosuppressive. The polynucleotide or antisense
CC oligonucleotide is useful for the manufacture of a medicament for
CC preventing, treating or ameliorating a medical condition, particularly
CC immune related disease, tumour, fungal infection or bacterial infection.
CC The immediate early IL-4 induced protein is useful for the manufacture of
CC a medicament for killing unwanted cells in a mammal. The antagonist is
CC useful for the manufacture of a medicament for use in decreasing cell
CC death. The polynucleotide is also useful for diagnosing a pathological
CC condition, particularly an immune related disease. These diseases may
CC include systemic lupus erythematosus, inflammatory bowel disease,
CC Guillain-Barre syndrome, Whipple's disease, atopic dermatitis, food
CC hypersensitivity, rheumatoid arthritis, osteoarthritis, diabetes mellitus
CC and psoriasis. The polynucleotide of the invention may be used in gene
CC therapy. The current sequence represents a human immediate early
CC interleukin-four induced protein. Note: This sequence should be encoded
CC by the DNA sequence given in the specification as SEQ ID 3 (Human
CC chromosome early interleukin-four induced protein genomic DNA from
CC chromosome 19q13.3-19q13.4 - see ABL56822), however, this does not appear
CC to be the case
XX
XX SQ Sequence 567 AA;

Query Match 37.0%; Score 999; DB 5; Length 567;
Best Local Similarity 41.8%; Pred. No. 1.8e-70;
Matches 217; Conservative 99; Mismatches 171; Indels 32; Gaps 9;

QY 3 LHVVKWKLVSVLITLYSHT-VALSLKEHLADCLDXYDTLLQTLNGLPHINTSHH 61
DB 6 LHL-----LVLPILLSVASODWKAERSQDPPEKCMQDPDYEQLLKVVTVWGLNRTLKQPR 61
QY 62 VVIVGAGMAGLTAALKLODAGHTVTILEANDRVGGRVETRYNEKEGWAEMGAMRIPSSH 121
DB 62 VIVVGAGVAGLVAAKVLSADGAKVTLEADNRIGGRIFTRDQNTGWIQELGAMRPPSSH 121
QY 122 RIYQWFKVLGVENNEFVMTDDNTFFLVNGVRERTYVQENPDVLKYNVSESEKGISADD 181
DB 122 RILHLKCGGLNLTKETQTDKNTWTEVHEVKLVNVVKEPKLGVYALRPQKGHSPED 181
QY 182 LLDPALQKVEEANGKAALEKYDRYSKVEYKKEGGSLSPGAVRMIGDLLNEQSLMYT 241
DB 182 IYQMALNQALKDKALGCRKAMKFFERTLLELLGEGNSRPAVQLLGDVMSDEGFFYL 241
QY 242 ALSEMIYDQADVNSVTYHEVTGSDLLPEAFSLVLDPIILLNSKVKHQRQSDKGIVSVY 301
DB 242 SFAALRAHSCLSRLQVSRIVGWDLLPRALLSGLVLLNAPVVMVMTQGHDPVHVQI 301
QY 302 QTGNES-SLMDLSADIVLVTTAKAALFIDFPPLSLSKWEALRSVHYDSSTKILITFRD 360
DB 302 ETSPPARNLKVLDKADVLLTAGSPAVKRIITFSPPLPRMQEALRRLHYVPATKVFLSFR 361
QY 361 KFWEDDGIKRGKSTGDPGRVIYYPSPHSFHTNETIGVLLASYTWSDESLLFLGASDBELK 420
DB 362 PFWEHEIEGGHSNDRPSRMIFYP-----PPREGALLLASYTWSDDAAAFAGLSREAL 416

QY 421 ELALRDLAKIHG---EQVWDKCTGVIVKWSADPYSGLGAFALFTPYQHLVYAQELFSSE- 476
DB 417 RLALDDVAALHGFVVRQLWDG-TGV-VKRWEDQHSQGGFVVQPP-----ALWQTEK 466
QY 477 -----GRVHFAGHTAPPHAWIETSMKSAIRAATNIN 508
DB 467 DDWTVPYGRIFYAGHTAYPHGCVETAVKSAALRAAKIN 505
RESULT 14
ABB95510
ID ABB95510 standard; protein; 567 AA.
XX AC ABB95510;
XX DT 19-JUL-2002 (first entry)
DE Human angiogenesis related protein PRO1265 SEQ ID NO: 176.
XX Human; angiogenesis; PRO protein; cardiovascularisation; wound; cancer;
XX atherosclerosis; cardiac hypertrophy; gene therapy; endothelial disorder;
KW cardiant; cytostatic; antiangiogenic; hypotensive; vulnerary;
KW antiarteriosclerotic.
XX OS Homo sapiens.
XX PN WO200208284-A2.
XX PD 31-JAN-2002.
XX 09-JUL-2001; 2001WO-US021735.
XX 20-JUL-2000; 2000US-0219556P.
XX 25-JUL-2000; 2000US-0220624P.
XX 25-JUL-2000; 2000US-0220664P.
XX 28-JUL-2000; 2000WO-US020710.
XX 02-AUG-2000; 2000US-0222695P.
XX 17-AUG-2000; 2000US-00643657.
XX 23-AUG-2000; 2000WO-US023522.
XX 24-AUG-2000; 2000WO-US023328.
XX 07-SEP-2000; 2000US-0230978P.
XX 18-SEP-2000; 2000US-00664610.
XX 18-SEP-2000; 2000US-00665350.
XX 24-OCT-2000; 2000US-0242922P.
XX 08-NOV-2000; 2000US-00709238.
XX 08-NOV-2000; 2000WO-US030952.
XX 10-NOV-2000; 2000WO-US030873.
XX 01-DEC-2000; 2000WO-US032578.
XX 20-DEC-2000; 2000US-00747259.
XX 22-DEC-2000; 2000WO-US034956.
XX 28-FEB-2001; 2001US-00767609.
XX 28-FEB-2001; 2001US-00796498.
XX 01-MAR-2001; 2001WO-US006520.
XX 09-MAR-2001; 2001US-00802706.
XX 14-MAR-2001; 2001US-00808689.
XX 22-MAR-2001; 2001US-00816744.
XX 05-APR-2001; 2001US-00828366.
XX 10-MAY-2001; 2001US-00854208.
XX 10-MAY-2001; 2001US-00854280.
XX 25-MAY-2001; 2001US-00866034.
XX 25-MAY-2001; 2001WO-US017092.
XX 30-MAY-2001; 2001US-00870574.
XX 30-MAY-2001; 2001WO-US017443.
XX 01-JUN-2001; 2001WO-US017800.
XX 20-JUN-2001; 2001WO-US019692.
XX (GETH) GENENTECH INC.
PA (BAKE/) BAKER K P.
PA (FERR/) FERRARA N.
PA (GERB/) GERBER H.

PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (MARS/) MARSTERS S A.
PA (PANJ/) PAN J.
PA (PAON/) PAONI N F.
PA (STEP/) STEPHAN J F.
PA (WATA/) WATANABE C K.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
XX
PI Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;
PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;
PI Stephan JF, Watanabe CK, Williams PM, Wood WJ, Ye W;
XX
DR WPI: 2002-171999/22.
DR N-PSDB; ABL95648.
XX
PT One hundred and eighty seven nucleic acids encoding PRO polypeptides,
PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial
PT infarction), endothelial or angiogenic disorders in a mammal.
XX
PS Claim 11; Fig 176; 567pp; English.
XX
CC The present invention provides the protein and coding sequences of human
CC PRO proteins. These are useful for treating or diagnosing a
CC cardiovascular, endothelial or angiogenic disorder, including cardiac
CC hypertrophy, trauma, cancer, age-related macular degeneration,
CC atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis,
CC angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour
CC angiogenesis (such as breast carcinoma and liver carcinoma) and wound
CC healing. The present sequence is a PRO protein of the invention
XX
SQ Sequence 567 AA;

Query Match 37.0%; Score 999; DB 5; Length 567;
Best Local Similarity 41.8%; Pred. No. 1.8e-70;
Matches 217; Conservative 99; Mismatches 171; Indels 32; Gaps 9;

QY 3 LHVWVKLSVSVSLTLYYSHT-VALSLKEHLADCLEKDYDTLLQTLNDGLPHINTSHH 61
DB 6 LHL-----LVLVILLSVASODWKAERSQDPPEKCMQDPDYEQLLKVVTVGLNRLTKPQR 61
QY 62 VIVGAGMAGLTAALKLODAGHTVTILANDRVGGRVETRYNEKEGVAENGAMRIPSSH 121
DB 62 VIVGAGVAGLVAAKVLSDAGHKVTILEADNRIGGRIFTYDQNTGWTGELGAMRMPSSH 121
QY 122 RIVQWFKVLGVEMNEFVMTDDNTFVLVNGVRRTYVYQENPDVLKYNVSESEKISADD 181
DB 122 RILHLKLCQGLGLNLTFTQYDKNTWTEVHEVKLVYVVEKPEKLGVALRPOEKHSPED 181
QY 182 LLDRALQKQKEVEANGKALEKVDYRSVKEYLKEEGGLSPGAVRMTGDLNLEQSLMYT 241
DB 182 IYQNALNQAALDKALGCRKAMKFERHTLLEYLLGEGNLSRPAVQLLDGVMSEDPFYL 241
QY 242 ALSEMIYDQADVNSVTVHEVTGSDLLPEAFSLVDVPIILNSKVYKHRSQDKGVIVSY 301
DB 242 SFABALRAHSCLSRQLQYSRIVGGWDLPLRALLSLGLVLLNAPVVAWMTQPHDVHVQI 301
QY 302 QTGNES-SLMDLSADIVLVTTTAKAALFIDFPDPLSISKMEALRSVHYDSTKILLTPRD 360
DB 302 ETSPPARNLKVLAADVLLTASGPAVKRITSPPLPRHQALRLRHVPAKVFSLSPRR 361
QY 361 KFWEDDGIRGKSGITDGPSPRYIYPSHFHNTETIGVLLASYSWDSLELLFLGASDEBLK 420
DB 362 PFWRREEHIEGHSNTDRSPRMIFYP-----PPREGALLASYSWDSAAAFAGLSREAL 416
QY 421 ELALRLAKING-----EQWDKCTGVIVKWSADPYSIGAFALFTPYQHLEYVAQBLFSE- 476
DB 417 RLALDDVAALHGPVVRQLWDG-TGV-VKRWAEODHQSOGFVVQPP-----ALWQTEK 466

QY 477 -----GRVHFAGEHTAPPHAWIETSMKSAIRAAATNIN 508
DB 467 DDWTPVYGRYIFAGEHTAYPHGWVETAVKSAALRAAIKIN 505

RESULT 15
ABO17853
ID ABO17853 standard; protein; 567 AA.
XX
AC ABO17853;
XX
DT 26-AUG-2003 (first entry)
XX
DE Novel human secreted and transmembrane protein PRO1265.
XX
KW Human; secreted and transmembrane protein; PRO; antiinflammatory;
KW antiarteriosclerotic; cardiant; anti-infertility; anti-HIV; cytostatic;
KW antidiabetic; gene therapy; tumour necrosis factor (TNF)-alpha release;
KW TNF-alpha release; cell proliferation; cell differentiation;
KW gene expression modulator; proteoglycan release; cytokine release;
KW tumour; inflammatory disease; organ failure; atherosclerosis;
KW cardiac injury; infertility; birth defect; premature aging; AIDS;
KW acquired immunodeficiency syndrome; cancer; diabetic complication;
KW chromosome mapping; gene mapping; pharmaceutical; diagnostic; biosensor;
KW bio-reactor; tissue typing.
XX
OS Homo sapiens.
XX
PN US2003032156-A1.
XX
PD 13-FEB-2003.
PP
PF 06-MAY-2002; 2002US-00140474.
XX
PR 31-MAR-1997; 97WO-US005230.
PR 12-JUN-1998; 98WO-US012456.
PR 14-JUL-1998; 98WO-US014552.
PR 28-AUG-1998; 98WO-US017888.
PR 10-SEP-1998; 98WO-US018824.
PR 14-SEP-1998; 98WO-US019093.
PR 14-SEP-1998; 98WO-US019094.
PR 14-SEP-1998; 98WO-US019177.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98WO-US019437.
PR 07-OCT-1998; 98WO-US021141.
PR 29-OCT-1998; 98WO-US022991.
PR 29-OCT-1998; 98WO-US022992.
PR 20-NOV-1998; 98WO-US024855.
PR 01-DEC-1998; 98WO-US025108.
PR 05-JAN-1999; 98WO-US000106.
PR 08-MAR-1999; 98WO-US005028.
PR 10-MAR-1999; 98WO-US005190.
PR 20-APR-1999; 98WO-US008615.
PR 14-MAY-1999; 98WO-US010733.
PR 02-JUN-1999; 98WO-US012252.
PR 01-SEP-1999; 98WO-US020111.
PR 08-SEP-1999; 98WO-US020594.
PR 13-SEP-1999; 98WO-US020944.
PR 15-SEP-1999; 98WO-US021090.
PR 15-SEP-1999; 98WO-US021547.
PR 05-OCT-1999; 98WO-US023089.
PR 29-NOV-1999; 98WO-US028214.
PR 30-NOV-1999; 98WO-US028313.
PR 30-NOV-1999; 98WO-US028409.
PR 01-DEC-1999; 98WO-US028301.
PR 01-DEC-1999; 98WO-US028634.
PR 02-DEC-1999; 98WO-US028551.
PR 02-DEC-1999; 98WO-US028564.
PR 02-DEC-1999; 98WO-US028565.
PR 16-DEC-1999; 98WO-US030095.
PR 20-DEC-1999; 98WO-US030911.
PR 20-DEC-1999; 98WO-US030999.
PR 22-DEC-1999; 98WO-US030720.

PR 30-DEC-1999; 99WO-US031243.
 PR 30-DEC-1999; 99WO-US031274.
 PR 05-JAN-2000; 2000WO-US000219.
 PR 06-JAN-2000; 2000WO-US000277.
 PR 06-JAN-2000; 2000WO-US000376.
 PR 11-FEB-2000; 2000WO-US003565.
 PR 18-FEB-2000; 2000WO-US004341.
 PR 18-FEB-2000; 2000WO-US004342.
 PR 22-FEB-2000; 2000WO-US004414.
 PR 24-FEB-2000; 2000WO-US004914.
 PR 24-FEB-2000; 2000WO-US005004.
 PR 01-MAR-2000; 2000WO-US005601.
 PR 02-MAR-2000; 2000WO-US005746.
 PR 10-MAR-2000; 2000WO-US005841.
 PR 10-MAR-2000; 2000WO-US006319.
 PR 15-MAR-2000; 2000WO-US006884.
 PR 20-MAR-2000; 2000WO-US007377.
 PR 21-MAR-2000; 2000WO-US007532.
 PR 30-MAR-2000; 2000WO-US008439.
 PR 17-MAY-2000; 2000WO-US013705.
 PR 22-MAY-2000; 2000WO-US014042.
 PR 30-MAY-2000; 2000WO-US014941.
 PR 02-JUN-2000; 2000WO-US015284.
 PR 28-JUL-2000; 2000WO-US020710.
 PR 11-AUG-2000; 2000WO-US022031.
 PR 23-AUG-2000; 2000WO-US023522.
 PR 24-AUG-2000; 2000WO-US023328.
 PR 08-NOV-2000; 2000WO-US030952.
 PR 10-NOV-2000; 2000WO-US030878.
 PR 01-DEC-2000; 2000WO-US032678.
 PR 20-DEC-2000; 2000US-00747259.
 PR 20-DEC-2000; 2000WO-US034956.
 PR 28-FEB-2001; 2001US-00796498.
 PR 28-FEB-2001; 2001US-00065520.
 PR 01-MAR-2001; 2001WO-US006666.
 PR 09-MAR-2001; 2001US-00802706.
 PR 14-MAR-2001; 2001US-00808689.
 PR 22-MAR-2001; 2001US-00816744.
 PR 05-APR-2001; 2001US-00828366.
 PR 10-MAY-2001; 2001US-00854208.
 PR 10-MAY-2001; 2001US-00854280.
 PR 18-MAY-2001; 2001US-00860216.
 PR 25-MAY-2001; 2001US-00866028.
 PR 25-MAY-2001; 2001US-00866034.
 PR 25-MAY-2001; 2001US-00710992.
 PR 01-JUN-2001; 2001US-00872035.
 PR 01-JUN-2001; 2001WO-US017800.
 PR 05-JUN-2001; 2001US-00874503.
 PR 14-JUN-2001; 2001US-00882636.
 PR 19-JUN-2001; 2001US-00886342.
 PR 20-JUN-2001; 2001WO-US019692.
 PR 21-JUN-2001; 2001US-00887879.
 PR 22-JUN-2001; 2001WO-US020116.
 PR 29-JUN-2001; 2001WO-US021066.
 PR 09-JUL-2001; 2001WO-US021735.
 PR 18-JUL-2001; 2001US-00908827.
 PR 06-AUG-2001; 2001US-00924419.
 PR 09-AUG-2001; 2001US-00927796.
 PR 16-AUG-2001; 2001US-00931836.
 PR 19-DEC-2001; 2001US-00028072.
 (GETH) GENENTECH INC.

XX Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
 PI Geritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
 PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WL, Zhang Z;
 XX WPI; 2003-341980/32.
 DR N-PSDB; ACD24090.

XX New secreted and transmembrane PRO nucleic acids, for treating
 PT inflammation, organ failure, atherosclerosis, cardiac injury,
 PT infertility, birth defects, premature aging, acquired immunodeficiency

PT syndrome (AIDS), or cancer.
 XX Claim 12; Fig 476; 660pp; English.
 XX The invention describes an isolated nucleic acid (I) comprising, or which
 CC has 80 % sequence identity to, or the full-length coding sequence of, one
 CC of 275 nucleotide sequences, and which encodes a corresponding
 CC polypeptide selected from 275 amino acid sequences, where all sequences
 CC are given in the specification. The polypeptide encoded by (I) is used to
 CC detect PRO polypeptides, link a bioactive molecule to a cell expressing a
 CC PRO polypeptide, modulate a biological activity of a cell, stimulate the
 CC release of tumour necrosis factor (TNF)-alpha from human blood, modulate
 CC the uptake of glucose or free fatty acid by cells, stimulate or inhibit
 CC the proliferation or differentiation of cells or gene expression,
 CC stimulate the release of proteoglycans, stimulate the release of cytokine
 CC from peripheral blood mononuclear cells, inhibit the binding of A-peptide
 CC to factor VIIa, or detect the presence of tumour in a mammal. The nucleic
 CC acid and polypeptide encoded by it, are useful for treating inflammatory
 CC diseases, organ failure, atherosclerosis, cardiac injury, infertility,
 CC birth defects, premature aging, acquired immunodeficiency syndrome
 CC (AIDS), cancer, or diabetic complications. The nucleic acid is useful as
 CC hybridisation probes, in chromosome and gene mapping, and in generating
 CC antisense RNA or DNA. The polypeptides are useful as pharmaceuticals,
 CC diagnostics, biosensors or bioreactors. Both are useful in tissue typing.
 CC This is the amino acid sequence of a novel human secreted and
 CC transmembrane PRO polypeptide
 XX Sequence 567 AA;

Query Match 37.0%; Score 999; DB 6; Length 567;
 Best Local Similarity 41.8%; Pred. No. 1.8e-70;
 Matches 217; Conservative 99; Mismatches 171; Indels 32; Gaps 9;

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 Db 6 LHL-----LVLVPIILSLVASQDWKAERSQDPFEKMQDPDYQLKLVTVGWLNLTKFQR 61
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 Db 62 VIVVAGVAGLVAALKVLSLDAGHKVTILEADNRIGRIFTYRDQNTGIGELGAMRMPSSH 121
 QY 122 RIVQWFKVLGVENEFWMTDDNTFYLVNGVRITYVQENPDVLKYNVSSEKISADD 181
 Db 122 RILHLKQLGLNLTKFTQYDKNTWTEVHEKLRNVYVKEVPEKLGVALRPOEKHSPED 181
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 Db 182 IYQALNQALKDLKALGCRKAMKFERHTLLEYLLGEGNLSRPVQLLDGVMSDEGFFYL 241
 QY 242 ALSEMIYDQADVNDVTVYHEVTGGSDLLPEAFSLVDLPVILLNSKVGHROSDKGVIVSY 301
 Db 242 SFAEALRAHSCLSRLQVSRIVGGWDLPLRALLSGLVLNAPVAVMTQPHDVHVOI 301
 QY 302 QTGNES-SLMDLSADIVLVTAKAALFIDPDPPLISKMEALRSVHYDSTKILLTFRD 360
 Db 302 ETSPPARNLKVLLKADVLLLTASGPAVKRITFSPPLPRHMQALRLRLHVPATKVLSPRR 361
 QY 361 KFWEDDGIKGGKSTTDGSPRIYVPSHSFHTNETIGVLLASVTWSDEILLFLGASDEELK 420
 Db 362 PFWEHEHIEGGHSNTDRSRMIFYP-----PPREGALLASVTWSDAFAAGLSREAL 416
 QY 421 ELALRDLAKIHG---EQWMDKCTGVIVKWSADPYSLGAFALFTPYQHLEVAQELFSSE- 476
 Db 417 RLALDDVAALHGPVVRQLWDG-TGV-VKRWAEQHSQGGFVVQPP-----ALWQTEK 466
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 Db 467 DDWTPVPIYRIYFAGEHTAIPHGWVETAVKSALRAAIKIN 505

Search completed: October 4, 2005, 14:03:38
 Job time : 170 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 4, 2005, 13:32:30 ; Search time 43 Seconds
(without alignments)
909.677 Million cell updates/sec

Title: US-10-645-094-1
Perfect score: 2703
Sequence: 1 MNLHVVKWKLVSVLITLY.....TNINKVANEESTIEHTKDEL 524

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: /cgn2_6/ptodata/1/1aa/5B_COMB.pep.*
3: /cgn2_6/ptodata/1/1aa/6A_COMB.pep.*
4: /cgn2_6/ptodata/1/1aa/6B_COMB.pep.*
5: /cgn2_6/ptodata/1/1aa/PCTUS_COMB.pep.*
6: /cgn2_6/ptodata/1/1aa/backfiles.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2703	100.0	524	3	US-09-230-388-1
2	2703	100.0	524	4	US-09-912-176-1
3	999	37.0	567	3	US-08-813-150-4
4	999	37.0	567	4	US-09-546-553-4
5	979.5	36.2	566	4	US-09-482-273-173
6	488.5	18.1	319	4	US-09-482-273-267
7	488.5	18.1	320	4	US-09-482-273-194
8	476	17.6	275	4	US-09-482-273-265
9	417	15.4	617	3	US-09-063-733A-46
10	417	15.4	617	3	US-09-063-733A-56
11	417	15.4	617	3	US-09-063-733A-57
12	417	15.4	617	3	US-09-063-733A-58
13	404	14.9	617	3	US-09-314-242-2
14	392	14.5	695	3	US-09-314-242-12
15	387	14.3	212	4	US-09-482-273-266
16	364.5	13.5	488	4	US-09-986-536-2
17	307	11.4	538	4	US-09-252-991A-16952
18	294	10.9	545	4	US-09-949-016-11442
19	283	10.5	527	1	US-08-132-168A-32
20	283	10.5	531	4	US-09-949-016-11443
21	258	9.5	733	3	US-09-073-587-3
22	211.5	7.8	458	4	US-09-328-352-7549
23	197.5	7.3	554	3	US-09-352-159-17
24	197.5	7.3	554	3	US-09-352-168-17
25	197.5	7.3	554	4	US-09-771-045B-17
26	197.5	7.3	554	4	US-09-770-564A-17
27	196.5	7.3	463	4	US-09-771-045B-51

28	195.5	7.2	463	4	US-09-771-045B-53	Sequence 53, Appl
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30	195	7.2	487	3	US-09-352-168-21	Sequence 21, Appl
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32	195	7.2	487	4	US-09-770-564A-21	Sequence 21, Appl
33	194.5	7.2	463	4	US-09-771-045B-49	Sequence 49, Appl
34	193.5	7.2	600	3	US-09-352-159-36	Sequence 36, Appl
35	193.5	7.2	600	3	US-09-352-159-38	Sequence 38, Appl
36	193.5	7.2	600	4	US-09-771-045B-36	Sequence 36, Appl
37	193.5	7.2	600	4	US-09-771-045B-38	Sequence 38, Appl
38	193.5	7.2	600	4	US-09-882-694B-23	Sequence 23, Appl
39	193.5	7.2	600	4	US-09-882-694B-25	Sequence 25, Appl
40	192.5	7.1	600	4	US-09-771-045B-33	Sequence 33, Appl
41	192.5	7.1	829	3	US-09-352-159-33	Sequence 33, Appl
42	192.5	7.1	829	3	US-09-352-168-33	Sequence 33, Appl
43	192.5	7.1	829	4	US-09-770-564A-33	Sequence 33, Appl
44	191.5	7.1	462	3	US-09-352-159-6	Sequence 6, Appl
45	191.5	7.1	462	3	US-09-352-159-8	Sequence 8, Appl

ALIGNMENTS

RESULT 1
US-09-230-388-1
; Sequence 1, Application US/09230388
; Patent No. 6291644
; GENERAL INFORMATION:
; APPLICANT: Iwamoto, Mitsunori; Jung, Sang-Keel
; TITLE OF INVENTION: NOVEL PROTEIN, ITS GENE, REAGENTS FOR INDUCING
; FILE REFERENCE: 4703/OF214
; CURRENT APPLICATION NUMBER: US/09/230.388
; PRIOR FILING DATE: 1999-01-22
; PRIOR APPLICATION NUMBER: PCT/JP98/02261
; PRIOR FILING DATE: 1998-05-22
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 1
; LENGTH: 524
; TYPE: PRT
; ORGANISM: Scomber japonicus
US-09-230-388-1

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Db	121	HRIVQVFKVLGV	EMNEFVMTDDNT	FVLVNGVRERTYV	QVNPVLYKNVSESEKIGAD 180	
Qy	181	DLDRALQKQKEE	VEANGCKAALEKDY	RSYKYLEKEGGIS	PGAVRMIGDLLNEQSLMY 240	
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Qy	301	YQTCNESSLMD	SADIVLVTAKAAL	FIDPDPPLSISK	MEALRSVHYDSSTKILLTFRD 360	
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||||| 421 ELALRDLAKIHGEQWMDKCTGVIVKWSADPYSLGAFALFTPYQHLEYVAQELFSSEGRVH 480
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RESULT 2
US-09-912-176-1
; Sequence 1, Application US/09912176
; Patent No. 6649739
; GENERAL INFORMATION:
; APPLICANT: Iwamoto, Mitsunori; Jung, Sang-kee
; TITLE OF INVENTION: NOVEL PROTEIN, ITS GENE, REAGENTS FOR INDUCING
; TITLE OF INVENTION: APAPTOSIS, AND ANTICANCER AGENTS
; FILE REFERENCE: 4703/0F214
; CURRENT APPLICATION NUMBER: US/09/912,176
; PRIOR FILING DATE: 2001-07-24
; PRIOR FILING DATE: 2001/07/24
; PRIOR APPLICATION NUMBER: US 09/230,388
; PRIOR FILING DATE: 1998-01-22
; PRIOR APPLICATION NUMBER: PCI/JP98/02261
; PRIOR FILING DATE: 1998-05-22
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 524
; TYPE: PRT
; ORGANISM: Scomber japonicus
US-09-912-176-1

Query Match 100.0%; Score 2703; DB 4; Length 524;
Best Local Similarity 100.0%; Pred. No. 3.6e-239;
Matches 524; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MNLVVVKVLSVSVLITLYSHTVALSLKEHLADCLEDKOYDTLLQTLDNGLPHINTSH 60
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DB 61 HVVIVGAGWAGLTAAKLLQDAGHTVTILEANDRVGRVETRYNEKEGVAENGAMRIPSS 120
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DB 121 HRIVQFVKVLGVENNEFVMTDDNTFYLNGVRERTYVVOENPDVLYKNVSESEKISAD 180
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RESULT 3
US-08-813-150-4
; Sequence 4, Application US/08813150
; Patent No. 6069229
; GENERAL INFORMATION:
; APPLICANT: Mueller, Christopher
; APPLICANT: Lebecque, Serge J.E.
; APPLICANT: Liu, Yong-Jun
; APPLICANT: Dowling, Lynette M.
; APPLICANT: Huffine, Constance M.
; APPLICANT: Gorman, Daniel M.
; TITLE OF INVENTION: MAMMALIAN PROTEINASES; OXIDOREDUCTASES;
; NUMBER OF SEQUENCES: 6
; TITLE OF INVENTION: RELATED REAGENTS
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/813,150
; FILING DATE: 07-MAR-1997
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: SP0693
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-852-9196
; TELEFAX: 650-496-1200
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 567 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-813-150-4

Query Match 37.0%; Score 999; DB 3; Length 567;
Best Local Similarity 41.8%; Pred. No. 9.3e-83;
Matches 217; Conservative 99; Mismatches 171; Indels 32; Gaps 9;

QY 3 LHVYVVKVLSVSVLITLYSHT-VALSLKEHLADCLEDKOYDTLLQTLDNGLPHINTSHH 61
DB 6 LHL-----LVLVPIILLSVASQDWKAERSQDPFEKCMQDPDYEQLLKVVTVWGLNLTLPOR 61
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; Sequence 4, Application US/09546553
; Patent No. 6518405
; GENERAL INFORMATION:
; APPLICANT: Mueller, Christopher
; APPLICANT: Lebecque, Serge J.E.
; APPLICANT: Liu Yong-Jun
; APPLICANT: Dowling, Lynette M.
; APPLICANT: Huffine, Constance M.
; APPLICANT: Gorman, Daniel M.
; TITLE OF INVENTION: MAMMALIAN PROTEINASES; OXIDOREDUCTASES;
; TITLE OF INVENTION: RELATED REAGENTS
; NUMBER OF SEQUENCES: 6

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Query Match      37.0%; Score 999; DB 4; Length 567;
Best Local Similarity 41.8%; Pred.No. 9.3e-83;
Matches 217; Conservative 99; Mismatches 171; Indels 32; Gaps 9;

Qy 3 LHVVKWKLVSVLITLYGHT-VALSLKKEHLADCLCEDKYDTLLQTLNGLPHINTSHH 61
6 LHL-----LVLPILLSVASQDKWAERSQDPFEKCMQDPDYEQLLKVVTVGLNRLTKPQ 61
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Qy	182	LLDLRALQKVEEBAANGCAALEKYDRYSVKYEIKKEGGLSPGAVRMIIGDLNQSMLYT	241
Db	182	IYQWALNQALKDLKALGCRKAMKFERHTLLEYLLGEGNLSRPAVOLLLGDVMSDEGFFYL	241
Qy	242	ALSEMIYDQADVDSVTYHETVCGSDLLPEAFSLVLDVPILILNSKVKHIRQSDKGVIYSY	301
Db	242	SFAELARHSCLSRLQYSRIVGWDLLPRALLSSGLVLNPAVWMTQPHDVHVOI	301
Qy	302	QTGNES-SLMDLSADIVLVTTTAKAALFIDPDPPLSISKMEALRSVHYDSSTKILLTFRD	360
Db	302	ETSPPARNLKVLKADVLLTASGPAVKRITFSPPLPRHMQEALRELHVVPATKVFLSFR	361
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Db	362	PFWREHEIBGHSNTRDPSRMIYPY-----PPREGALLASYTWSDAAAFAAGLSREEL	416
Qy	421	ELALRDLAKTHG--EQWQKCTGVIKKWSADPYSLGAFALFTPYQHLEYAQELFSSB-	476
Db	417	RLALDDVAALHGPVROLWNG-TGV-VKRWAEODHSGGFFVQVP-----ALWQTEK	466
Qy	477	-----GRVHPAGEHTAFPHAMTETSMKSIRAATNIN	508
Db	467	DDWTPVGRYIFYAGEHTAYPHGWVETAVKSAALRAAIKIN	505

```

RESULT 5
US-09-482-273-173
; Sequence 173, Application US/09482273
; Patent No. 6534631
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 71 Human Secreted Proteins
; FILE REFERENCE: P203091
; CURRENT APPLICATION NUMBER: US/09/482,273
; CURRENT FILING DATE: 2000-01-13
; EARLIER APPLICATION NUMBER: PCT/US99/15849
; EARLIER FILING DATE: 1999-07-14
; EARLIER APPLICATION NUMBER: 60/092,921
; EARLIER FILING DATE: 1998-07-15
; EARLIER APPLICATION NUMBER: 60/092,922
; EARLIER FILING DATE: 1998-07-15
; EARLIER APPLICATION NUMBER: 60/092,956
; EARLIER FILING DATE: 1998-07-15
; NUMBER OF SEQ ID NOS: 267
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 173
; LENGTH: 566
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-482-273-173

```

[illegible]

Db 122 RILHLKCOGLGLNLTKFTQYDKNTWTEVHEVKLRNVVVEKPEKLGVALRQEKGHSPED 181
Qy 182 LLDRLALQKVEEANGCAALEKYDRYSVKEYLKEBGLSPGAVRMTGDLNLSQSLMYT 241
Db 182 IQMALNQALKDLKALGCRKAMKFERHTLLEYLLGEGNLSRPAVQLLGDVMSDGGFFYL 241
Qy 242 ALSEMIYDQADVNDSTVTHEVTGSDLLPEAFSLVLDVPIILNSKVKHQSDKGIVSY 301
Db 242 SPAEALRAHSCLSDRLOYSRIVGGWDLPRALLSSLSGLVLLNAPVAVMTQGPDHVHVOI 301
Qy 302 QTGNES-SLMDLSADIVLVTAKAALFIDFDPPLSISKMAALRSVHYDSSTKILLTPRD 360
Db 302 ETSPPARNLKVLKADVLLTASGPAVKRITSPPLPRHQEALRLHYVPATKVFLSFRR 361
Qy 361 KEWEDDGIRGKSIITDGPSTRIYYPSPHFTNETTGVLLASVTSDESLLFLGASDEBLK 420
Db 362 PFWREHIEBGCHSNTDRPSRMIFYP-----PPREGALLASVTSDDAAAFAGLSREBAL 416
Qy 421 ELALRDLAKIHG---EQWDKCTGVIVKWSADPYSLSGAFALFTPYQHLEYAQELFSSE- 476
Db 417 RLALDDVAALHGFVVRQLWDG-TGV-VKRWAEQHSQGFVVOPP-----ALWQTEK 466
Qy 477 -----GRVHPAGEHTAPPHAWIETSMKSALRAATNIN 508
Db 467 DDMVTPYGRIFYAGEHTAYPHGCVETAVK-LLRAAIKIN 504

RESULT 6
US-09-482-273-267
; Sequence 267, Application US/09482273
; Patent No. 6534631
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 71 Human Secreted Proteins
; FILE REFERENCE: P2030P1
; CURRENT APPLICATION NUMBER: US/09/482,273
; EARLIER FILING DATE: 2000-01-13
; EARLIER APPLICATION NUMBER: PCT/US99/15849
; EARLIER FILING DATE: 1999-07-14
; EARLIER APPLICATION NUMBER: 60/092,921
; EARLIER FILING DATE: 1998-07-15
; EARLIER APPLICATION NUMBER: 60/092,922
; EARLIER FILING DATE: 1998-07-15
; EARLIER APPLICATION NUMBER: 60/092,956
; EARLIER FILING DATE: 1998-07-15
; NUMBER OF SEQ ID NOS: 267
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 267
; LENGTH: 319
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (68)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (115)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (213)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (320)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-482-273-267

Query Match 18.1%; Score 488.5; DB 4; Length 319;
Best Local Similarity 33.6%; Pred. No. 2.5e-36;
Matches 112; Conservative 69; Mismatches 109; Indels 43; Gaps 4;
Qy 3 LHVVKWKLSSVSVLITLYSHT-VALSLKEHLADCLDCKDYDTLLQTLNDGLPHINTSHH 61
Db 6 LHL-----LVLVPILLSLVASQDWKERSQDPFEKCMQDPDYEQLLK----- 47

Qy 62 VVIVGAGMAGLTAALKLQDAGHTVTILEANDRVGGRVETVRYNEKEGVAEMGAMRIPSSH 121
Db 48 -----VTILEADNRIGGRIFTYRDQXTGWIIGELGAMRPSSH 84
Qy 122 RIVQWFKVLGVEMNEFVMTDDNTFYLVNGVRERTTVVQENPDVLKYNVSESEKGISADD 181
Db 85 RILHLKCOGLGLNLTKFTQYDKNTWTEVHEVKLRNVVVEKPEKLGVALRQEKGHSPED 144
Qy 182 LLDRLALQKVEEANGCAALEKYDRYSVKEYLKEBGLSPGAVRMTGDLNLSQSLMYT 241
Db 145 IQMALNQALKDLKALGCRKAMKFERHTLLEYLLGEGNLSRPAVQLLGDVMSDGGFFYL 204
Qy 242 ALSEMIYDQADVNDSTVTHEVTGSDLLPEAFSLVLDVPIILNSKVKHQSDKGIVSY 301
Db 205 SPAEALRAHSCLSDRLOYSRIVGGWDLPRALLSSLSGLVLLNAPVAVMTQGPDHVHVOI 264
Qy 302 QTGNES-SLMDLSADIVLVTAKAALFIDFDP 333
Db 265 ETSPPARNLKVLKADVLLTASGPAVKRITFSP 297

RESULT 7
US-09-482-273-194
; Sequence 194, Application US/09482273
; Patent No. 6534631
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 71 Human Secreted Proteins
; FILE REFERENCE: P2030P1
; CURRENT APPLICATION NUMBER: US/09/482,273
; EARLIER FILING DATE: 2000-01-13
; EARLIER APPLICATION NUMBER: PCT/US99/15849
; EARLIER FILING DATE: 1999-07-14
; EARLIER APPLICATION NUMBER: 60/092,921
; EARLIER FILING DATE: 1998-07-15
; EARLIER APPLICATION NUMBER: 60/092,922
; EARLIER FILING DATE: 1998-07-15
; EARLIER APPLICATION NUMBER: 60/092,956
; EARLIER FILING DATE: 1998-07-15
; NUMBER OF SEQ ID NOS: 267
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 194
; LENGTH: 320
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (68)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (115)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (213)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (320)
; OTHER INFORMATION: Xaa equals stop translation
US-09-482-273-194

Query Match 18.1%; Score 488.5; DB 4; Length 320;
Best Local Similarity 33.6%; Pred. No. 2.6e-36;
Matches 112; Conservative 69; Mismatches 109; Indels 43; Gaps 4;
Qy 3 LHVVKWKLSSVSVLITLYSHT-VALSLKEHLADCLDCKDYDTLLQTLNDGLPHINTSHH 61
Db 6 LHL-----LVLVPILLSLVASQDWKERSQDPFEKCMQDPDYEQLLK----- 47
Qy 62 VVIVGAGMAGLTAALKLQDAGHTVTILEANDRVGGRVETVRYNEKEGVAEMGAMRIPSSH 121

Db 48 -----VTILEADNRIGGRIFTYRDQXTGWI GELGAMRPPSH 84
Qy 122 RIVQWFKKLGVMNEFVMTDNTFYLVNGVRERTYVVOENPDVLKYNVSESEKGISADD 181
Db 85 RIHLKLCQGLNLTKFTQYDKNVTVEVHEXKLRLNVVVEKPEKGLGYALRPOEKGHSPED 144
Qy 182 LDLRALQKVEEVEANGCKAALEKYDRYSVKEYLKEBEGGLSPGAVRMIGDNLNEOSLMYT 241
Db 145 IYQMALNQALKOLKALGCRKAMKKFERHTLLEYLLEGGNLSRPAVOLLDGVMSEDDGFFYL 204
Qy 242 ALSEMIYDQADVNDVSYVYHEVTVGGSDLLPEAFSLVDVPILLNSKVYKHRSQDKGVIVSY 301
Db 205 SPAEALRAXSCUSDRLQYBRIYVGGWDLPRALLSSLSGLVLLNAPVAMTQGPHDVHQI 264
Qy 302 QTGNES-SLMDLSADIVLVTTAKAALFIDFDP 333
Db 265 ETSPPARNLKVLKADVLLTASGPAVKRITTFSP 297

RESULT 8

US-09-482-273-265
; Sequence 265, Application US/09482273
; Patent No. 6534631
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 71 Human Secreted Proteins
; FILE REFERENCE: P2030P1
; CURRENT APPLICATION NUMBER: US/09/482,273
; EARLIER FILING DATE: 2000-01-13
; EARLIER APPLICATION NUMBER: PCT/US99/15849
; EARLIER FILING DATE: 1999-07-14
; EARLIER APPLICATION NUMBER: 60/092,921
; EARLIER FILING DATE: 1998-07-15
; EARLIER APPLICATION NUMBER: 60/092,922
; EARLIER FILING DATE: 1998-07-15
; EARLIER APPLICATION NUMBER: 60/092,956
; EARLIER FILING DATE: 1998-07-15
; NUMBER OF SEQ ID NOS: 267
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 265
; LENGTH: 275
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (47)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (94)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (192)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-482-273-265

Query Match 17.6%; Score 476; DB 4; Length 275;
Best Local Similarity 34.7%; Pred. No. 2.8e-35;
Matches 103; Conservative 62; Mismatches 94; Indels 38; Gaps 2;
Qy 36 CLEDKDYDTLLQTLONGPLHINTSHHVIVGAGMAGLTAALKLQDAGHTVTILEANDRVG 95
Db 15 CMQDPDYEQLK-----VTILEADNRIG 37
Qy 96 GRVETRYNEKEGWYAEAMGARIPSSHRIVQWFKKLGVMNEFVMTDNTFYLVNGVRER 155
Db 38 GRIFTYRDQXTGWI GELGAMRPPSHRIHLKLCQGLNLTKFTQYDKNVTVEVHEXKL 97
Qy 156 TVVVOENPDVLKYNVSESEKGISADDLLDRALQKVEEVEANGCKAALEKYDRYSVKYL 215
Db 98 NYVVEKVPKGLYALRPOEKGHSPEDIYQMALNQALKOLKALGCRKAMKKFERHTLLEYL 157

Qy 216 KEEGGLSPGAVRMIGDNLNEOSLMYALSEMIYDQADVNDVSYVYHEVTVGGSDLLPEAFUS 275
Db 158 LLEGNLSRPAVOLLDGVMSEDDGFFYLSFAEALRAXSCLSDRLQYSRIVGGWDLPRALLS 217
Qy 276 VLDVPILLNSKVYKHRSQDKGVIVSYQTGNES-SLMDLSADIVLVTTAKAALFIDF 331
Db 218 SLSGLVLLNAPVAMTQGPHDVHQIETSPARNLKVLKADVLLTASGPAVKRITTF 274

RESULT 9

US-09-063-733A-46
; Sequence 46, Application US/09063733A
; Patent No. 6372211
; GENERAL INFORMATION:
; APPLICANT: Isaac, Barbara G.
; APPLICANT: Greenplate, John T.
; APPLICANT: Purcell, John P.
; APPLICANT: Romano, Charles P.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR CONTROLLING
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold White & Durkee
; STREET: PO Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/063,733A
; FILING DATE: 21-APR-1998
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Patterson, Melinda L.
; REGISTRATION NUMBER: 33,062
; REFERENCE/DOCKET NUMBER: MOBT:022
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713-787-1400
; TELEFAX: 713-787-1440
; INFORMATION FOR SEQ ID NO: 46:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 617 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
US-09-063-733A-46

Query Match 15.4%; Score 417; DB 3; Length 617;
Best Local Similarity 31.0%; Pred. No. 2.7e-29;
Matches 156; Conservative 83; Mismatches 177; Indels 88; Gaps 26;
Qy 62 VVIWAGMAGLTAALKLQD---AGHTVTILEANDRVGGRVET--YRNEKEGWYAEWGMAR 116
Db 87 VCIWAGVSGUYIAMIILDDDLKIPNLTYDIFESSRGTGRLYTHHTFDKADHYI-DIGAMR 145
Qy 117 ---IPSSHRIVQWFKKLGVMNEFVMTDNTFYLVN-----GYRERTYVVOENPDVLK 167
Db 146 YPDIPSMKRTNLF-KRTGMPLIKYLDGENTPOLYNNHFFAKGVSD-----P 192
Qy 168 YNVSESEKGISADDLLDRALQKV-----KEEVEANGCKA--ALEKYDRYSVKYLYKEE 218
Db 193 YMWVANGGTVPDWDVDSVSGEKLOQAFGYKKEKLAEDPKGFDELMLVDDMTTREYLKRG 252
Qy 219 G--GLSPG----AVRMIGDNLNEOSLMYALSEMIYDQADVNDV--TYHEVTVGGSDLLP 270
Db 253 GPKGEAPKYDFPAIQWMTQTNTGNLFDQAFSEVSDSFDPNPTKPEWYCIEGTSLLV 312
Qy 271 EAFSLVDVPILLNSKVKHIR----QSKDGIVSYQTGNESLSMDLSADIVLVTTAKAA 326

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Db 313 DAMKETLVHKVQNNKRVDAISIDLDPDGG-NMSVRIGGK-----DHSGYSTVFNTTALGC 367
Qy 327 L-----FIDPDPPLSISKMEALRSVHYDSSTKILLTPRDKFW-EDDGIR-GGKSITDGP 378
Db 368 LDRMDLRGLNLHP-----TQADAIRCLHYDNSTKVALKESYFWWIKDCGICITCGGAATDLP 423
Qy 379 SRYIYPPSHSF-HTNETIGVLLASYTWSDESLLFLGA-----SDEELKELALRDL 427
Db 424 LRTCVYPSNLDLTGE--AVLLASYTWSQDATR-IGSLVKDAPPQPPKEDLVELILQNL 480
Qy 428 AKIHG-----EQWMDKCTGVI-VKWSADPYSLGAFALFTPYOHLEVAQELF--SSSEGRV 479
Db 481 ARLHAEMTYEKIKEAYTGVYHAYCWANDPNVGGAFALFGPGQFSNLYPYLMRPAAGGKF 540
Qy 480 HFAEHTAPFHAMWETSMSKAIRA 503
Db 541 HIVEASSVHHAWIIGSLESAYTA 564

RESULT 10
US-09-063-733A-56
; Sequence 56, Application US/09063733A
; Patent No. 6372211
; GENERAL INFORMATION:
; APPLICANT: Isaac, Barbara G.
; APPLICANT: Greenplate, John T.
; APPLICANT: Purcell, John P.
; APPLICANT: Romano, Charles P.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR CONTROLLING
; TITLE OF INVENTION: INSECTS
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold White & Durkee
; STREET: PO Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/063,733A
; FILING DATE: 21-APR-1998
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Patterson, Melinda L.
; REGISTRATION NUMBER: 33,062
; REFERENCE/DOCKET NUMBER: MOBT:022
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713-787-1400
; TELEFAX: 713-787-1440
; INFORMATION FOR SEQ ID NO: 56:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 617 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; US-09-063-733A-56

Query Match 15.48; Score 417; DB 3; Length 617;
Best Local Similarity 31.08; Pred. No. 2.7e-29;
Matches 156; Conservative 83; Mismatches 177; Indels 88; Gaps 26;

Qy 62 VVIWAGMAGITAAKLQD---AGHTVTILEANDRVGGRVET--YRNEKEGMYAENGAMR 116
Db 87 VCIVGAGVSGLYIAMILDLKIPNLTYDIFESSRGTGRLYTHHFTDAKHDIY-DIGAMR 145
Qy 117 ---IPSSHRIVQWFKVLGEMEFVMTDDNTFVLN-----GVERTYVQVENFDVLK 167

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Db 146 YPDI PSMKETNLF-KRTGMPLIKYYLDGENTPQLVNNHFFAKGVSD-----P 192
Qy 168 YNVSESEKISADLLDRALQV-----KEEVEANGCKA--ALEKYDRYSVKEYLKEE 218
Db 193 YWVSVANGGTVPDDVVDSVGEKLLQQAAGYGYKELABDFDKGDFELMLVDDMTTRELKRG 252
Qy 219 G--GLSPG---AVRMIGDLLNEQSLMYTALSEMIYDQADVNDV--TYHEVTGGSDLLP 270
Db 253 GPGEAPKYDFFAIOOMETQNTGTLFDOAFSESVIDSFDFDNPTKPEWYCIEGGTSLLV 312
Qy 271 EAFSLVDLPILLNSKVHIR-----QSDKGVIVSYOTGNESSLMDSADILVLTAKAA 326
Db 313 DAMKETLVHKVQNNKRVDAISIDLDPDGG-NMSVRIGGK-----DHSGYSTVFNTTALGC 367
Qy 327 L-----FIDPDPPLSISKMEALRSVHYDSSTKILLTPRDKFW-EDDGIR-GGKSITDGP 378
Db 368 LDRMDLRGLNLHP-----TQADAIRCLHYDNSTKVALKESYFWWIKDCGICITCGGAATDLP 423
Qy 379 SRYIYPPSHSF-HTNETIGVLLASYTWSDESLLFLGA-----SDEELKELALRDL 427
Db 424 LRTCVYPSNLDLTGE--AVLLASYTWSQDATR-IGSLVKDAPPQPPKEDLVELILQNL 480
Qy 428 AKIHG-----EQWMDKCTGVI-VKWSADPYSLGAFALFTPYOHLEVAQELF--SSSEGRV 479
Db 481 ARLHAEMTYEKIKEAYTGVYHAYCWANDPNVGGAFALFGPGQFSNLYPYLMRPAAGGKF 540
Qy 480 HFAEHTAPFHAMWETSMSKAIRA 503
Db 541 HIVEASSVHHAWIIGSLESAYTA 564

RESULT 11
US-09-063-733A-57
; Sequence 57, Application US/09063733A
; Patent No. 6372211
; GENERAL INFORMATION:
; APPLICANT: Isaac, Barbara G.
; APPLICANT: Greenplate, John T.
; APPLICANT: Purcell, John P.
; APPLICANT: Romano, Charles P.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR CONTROLLING
; TITLE OF INVENTION: INSECTS
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold White & Durkee
; STREET: PO Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/063,733A
; FILING DATE: 21-APR-1998
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Patterson, Melinda L.
; REGISTRATION NUMBER: 33,062
; REFERENCE/DOCKET NUMBER: MOBT:022
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713-787-1400
; TELEFAX: 713-787-1440
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 617 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; US-09-063-733A-57

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Query Match 15.4%; Score 417; DB 3; Length 617;
Best Local Similarity 31.0%; Pred. No. 2.7e-29;
Matches 156; Conservative 83; Mismatches 177; Indels 88; Gaps 26;

QY 62 VVIVGAGMAGLTAALKLQD---AGHTVTTILEANDRVGGRVET--YRNEKEGHYAENGAMR 116
DB 87 VCVIVGAGVGLYIAMILDDLKIPNLTYDIFESSRTGGRLYTHHFTDAKHYY-DIGAMR 145
QY 117 ---IPSSHRIVQWFKLVGMNEFVMTDDNTFYLVN-----GVRERTYVVQENPDVLK 167
DB 146 YPDIPSMKRTNLP-KRTGMPLEIKYLDGENTPOLYNNHFFAKGVSD-----P 192
QY 168 YNVSESEKISADLLDRALQV-----KEEVEANGCKA--ALEKYDRYSVKYELKEE 218
DB 193 YMVSVANGGTVPDDVVDVSVGEKQQAFGYKKEKLAEDFKGFDELMLVDDMTTREVLYKRG 252
QY 219 G--GLSPG---AVRMIGDLLNEQSLMYTALSEMIYDQADVNSV--TYHEVTGSDLLP 270
DB 253 GPKGEAPKYDFFAIQMMETQNTGTLNLFDOAFSESVIDSFDFNPTKPEWYCIEGGTSLLV 312
QY 271 EAFSLVDVPIILLNSKVKHIR---QSDKGIVSVYOTGNESSLMDSLADIVLVTTTAKAA 326
DB 313 DAMKETLVHKVQNNKRVDAISIDLAPDDG--NMSVRIGGK-----DHSGYSTVNTTALGC 367
QY 327 L-----FIDFPPPLSISKMEALRSVHYDSSTKILLTFRDKFW--EDDGIR--GGKSITDGP 378
DB 368 LDRMDLRGLNLHP---TQADAIRCLHYDNSTKVALKFSYPWWIKDCGTCGGAASDLP 423
QY 379 SRYIYYPHSHP-HTNETIGVLLASTYWSDESLLFLGA-----SDEELKELALRDL 427
DB 424 LRTCVPYSNLDGTGE--AVLLASTYWSQDATR--IGSLVKDAPPQPPKEDLVELILQNL 480
QY 428 AKIHG-----EOVMDKCTGVI--VKKWSADPYSLGAFALFPTPYQHLEYAQELF--SSEGRV 479
DB 481 ARLHAHMTYEKIKEAYTGVIHAYCWANDPNVGGAFALFGPGQFNSLYPYLMRPAAGKGF 540
QY 480 HFAGEHTAFPHAWIETSMKSIRA 503
DB 541 HIVGEASSVHHAWIIGSLESAYTA 564
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```
RESULT 12
US-09-063-733A-58
; Sequence 58, Application US/09063733A
; Patent No. 6372211
; GENERAL INFORMATION:
; APPLICANT: Isaac, Barbara G.
; APPLICANT: Greenplate, John T.
; APPLICANT: Purcell, John P.
; APPLICANT: Romano, Charles P.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR CONTROLLING
; NUMBER OF INVENTIONS: INSECTS
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold White & Durkee
; STREET: PO Box 4433
; CITY: Houston
; STATE: TX USA
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/063,733A
; FILING DATE: 21-APR-1998
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Patterson, Melinda L.
; REGISTRATION NUMBER: 33,062
```

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REFERENCE/DOCKET NUMBER: MOBT:022
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713-787-1400
TELEFAX: 713-787-1440
INFORMATION FOR SEQ ID NO: 58:
SEQUENCE CHARACTERISTICS:
LENGTH: 617 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
US-09-063-733A-58

Query Match 15.4%; Score 417; DB 3; Length 617;
Best Local Similarity 31.0%; Pred. No. 2.7e-29;
Matches 156; Conservative 83; Mismatches 177; Indels 88; Gaps 26;

QY 62 VVIVGAGMAGLTAALKLQD---AGHTVTTILEANDRVGGRVET--YRNEKEGHYAENGAMR 116
DB 87 VCVIVGAGVGLYIAMILDDLKIPNLTYDIFESSRTGGRLYTHHFTDAKHYY-DIGAMR 145
QY 117 ---IPSSHRIVQWFKLVGMNEFVMTDDNTFYLVN-----GVRERTYVVQENPDVLK 167
DB 146 YPDIPSMKRTNLP-KRTGMPLEIKYLDGENTPOLYNNHFFAKGVSD-----P 192
QY 168 YNVSESEKISADLLDRALQV-----KEEVEANGCKA--ALEKYDRYSVKYELKEE 218
DB 193 YMVSVANGGTVPDDVVDVSVGEKQQAFGYKKEKLAEDFKGFDELMLVDDMTTREVLYKRG 252
QY 219 G--GLSPG---AVRMIGDLLNEQSLMYTALSEMIYDQADVNSV--TYHEVTGSDLLP 270
DB 253 GPKGEAPKYDFFAIQMMETQNTGTLNLFDOAFSESVIDSFDFNPTKPEWYCIEGGTSLLV 312
QY 271 EAFSLVDVPIILLNSKVKHIR---QSDKGIVSVYOTGNESSLMDSLADIVLVTTTAKAA 326
DB 313 DAMKETLVHKVQNNKRVDAISIDLAPDDG--NMSVRIGGK-----DHSGYSTVNTTALGC 367
QY 327 L-----FIDFPPPLSISKMEALRSVHYDSSTKILLTFRDKFW--EDDGIR--GGKSITDGP 378
DB 368 LDRMDLRGLNLHP---TQADAIRCLHYDNSTKVALKFSYPWWIKDCGTCGGAASDLP 423
QY 379 SRYIYYPHSHP-HTNETIGVLLASTYWSDESLLFLGA-----SDEELKELALRDL 427
DB 424 LRTCVPYSNLDGTGE--AVLLASTYWSQDATR--IGSLVKDAPPQPPKEDLVELILQNL 480
QY 428 AKIHG-----EOVMDKCTGVI--VKKWSADPYSLGAFALFPTPYQHLEYAQELF--SSEGRV 479
DB 481 ARLHAHMTYEKIKEAYTGVIHAYCWANDPNVGGAFALFGPGQFNSLYPYLMRPAAGKGF 540
QY 480 HFAGEHTAFPHAWIETSMKSIRA 503
DB 541 HIVGEASSVHHAWIIGSLESAYTA 564
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RESULT 13
US-09-314-242-2
; Sequence 2, Application US/09314242A
; Patent No. 6248575
; GENERAL INFORMATION:
; APPLICANT: Elizabeth J. Golightly
; TITLE OF INVENTION: Nucleic Acids Encoding Polypeptides
; TITLE OF INVENTION: Having L-Amino Acid Oxidase Activity
; FILE REFERENCE: 5556,200-US
; CURRENT APPLICATION NUMBER: US/09/314,242A
; CURRENT FILING DATE: 1999-05-18
; EARLIER APPLICATION NUMBER: 09/080,428
; EARLIER FILING DATE: 1998-05-18
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 617
; TYPE: PRT
; ORGANISM: Trichoderma harzianum
US-09-314-242-2
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Query Match 14.9%; Score 404; DB 3; Length 617;
Best Local Similarity 30.6%; Pred. No. 4.2e-28;
Matches 154; Conservative 84; Mismatches 178; Indels 88; Gaps 26;

QY 62 VVVGAGMAGTAAKLLQD---AGHTVILEANDRVGRVET--YRNEKEGWYBMGAMR 116
DB 87 VCIVGAGVGLYIAMILDKIPNLTYDIFESSRRTGRLVTHHPTDAKHYY-DIGAMR 145
QY 117 ---IPSSHRIQVFWFKLGVENNEFVMTDDNTFYLVN-----GYRETYVVQENPDVLK 167
DB 146 YPDIPSMKRTFNLF-KRTKMPLIKYLKYGENTPQLYNNHFFAKGVSD-----P 192
QY 168 YNVSESEKISADLLDRALQKV-----KEVEANGCKA-ALEKYDYSVKYELKEE 218
DB 193 YNVSVANGTVPDDVDSVGEKLQAQFGYYKEKLAEDFKGDELMVLVDDMTREYLKRG 252
QY 219 G-GLSPG-----AVRMIGDLNLEQSLMTALSEMITYDOADVNSV--TYHEVTGSGDLLP 270
DB 253 GPKGEAPKYDFFAIQWMETQNTGTNLFDAFSESVIDSFDFDNPTKPEWYCIEGGTSLLV 312
QY 271 EAFSLVLDVPIILLNSKVHRIH---QSDKGVIVSYQTGNESLMDLSADIVLVTAKAA 326
DB 313 DAMEKTLVHKVQNNKRVDAISIDLDPDGG-NMSVRIGGK-----BHSGYSTVFNTALGC 367
QY 327 L-----FIDFPPLSISKMEALRSVHYDSSTKILLTFRDKFW-BDDGIR-GGKSITDGP 378
DB 368 LDRMDLRGLNHP-----TQADAIRCLHYDNSTKVALKESYPWIKDCGTCGGAASDLP 423
QY 379 SRYIYVPSHSF-HTNETIGVLASVTSWSESLFLGA-----SDEELKELALRDL 427
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QY 428 AKIHG-----EQWDKCTGVI-VKWSADPYSLGAFALFTPYQHLEYAQELF--SSEGRV 479
DB 481 ARLHAHMTYKIKAYTGVHAYCWANDPNVGGAFALFGPGQFQSNLYPYLMRPAAGKGF 540
QY 480 HFAGEHTAPPHAWIETSMKSALRA 503
DB 541 HVGASSVHHAWIGSLAESAYTA 564

RESULT 14
US-09-314-242-12
; Sequence 12, Application US/09314242A
; Patent No. 6248575
; GENERAL INFORMATION:
; APPLICANT: Elizabeth J. Golightly
; TITLE OF INVENTION: Nucleic Acids Encoding Polypeptides
; FILE REFERENCE: Having L-Amino Acid Oxidase Activity
; CURRENT APPLICATION NUMBER: US/09/314,242A
; CURRENT FILING DATE: 1999-05-18
; EARLIER APPLICATION NUMBER: 09/080,428
; EARLIER FILING DATE: 1998-05-18
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 12
; LENGTH: 695
; TYPE: PRT
; ORGANISM: Trichoderma harzianum
US-09-314-242-12

Query Match 14.5%; Score 392; DB 3; Length 695;
Best Local Similarity 27.0%; Pred. No. 6.4e-27;
Matches 148; Conservative 90; Mismatches 195; Indels 116; Gaps 26;

QY 37 LEDKDYDTLLQDLNGLPHINTSHVVIAGMAGTAAKLIQDAGHT-VTILEANDRVG 95
DB 160 LEDKE-----ISIVD---VEKAKSKNIAIVGAGMSGLMYLCITQAGMNVSIIEGNRLG 212
QY 96 GRVET-----YRNEKEGWYBMGAMRIP-----SSHRIV----- 124

DB 213 GRVHTEYLSGPPFDYS-----YQEMGPMRFPNTITLGNETYNVSDHQLVQLAEEMNSL 266
QY 125 QWFVKKLGVENNEFVMTDDNTFYLVNGVRETYVVQENPDV-LKYNVSESEKISADLL 183
DB 267 NGHSKNLSVDFIPWQNSNGLYYDGIK-----NPETGLPPTLAE-----LAANSSL 314
QY 184 DRALQKVEEVEANGCKAALEKYDRI--SVKEYLKE-----EGGLSPGAVRMIGDL 232
DB 315 --ALTRYSN---NSTKSLSQKVDAPLPTDKFLAEMAQNMKAHADWLSGGLAGLPDQ 368
QY 233 LNEOSLMTALSEMITYDOADVNSVT-----YHEVTGSDLLPEAFLSVL 277
DB 369 WSEFGFVNVLRGSLNDTAFAPALTGTCTRGCTFPRRRGAIDGGLNRLPLSFHPLV 428
QY 278 DVPILLNSKVHGI---RQSDKGVV---VSYQTGNESLMDLSADIVLVTAKAALFIDF 331
DB 429 DNATTLNRLRERAFDAETQKVTLHSRNSYKDSFESS-----EHDYAVIAAFSIVKKWRF 484
QY 332 DPPLSISK--MEALRSVHYDSSTKILLTFRDKFEW--DDGIRGGKSIT-DGPS-RYIYY 384
DB 485 SPALDLTAPTLANAIONLEYTSACKVALEFRTRFWEHLQPPIYVSGSCTSDIPGIGSICY 544
QY 385 PSHSFHNETIGVLLASY-----TWSDESLLFLGASDEELKELALDLAKIHGEQ-VWDKC 439
DB 545 PSYNINGTDPASTLASIYISGADWGRD---WVSTPEBEHVQYVLNAMAIIHGEELVKQSY 601
QY 440 TGVIVKK-WSADPYSLGAFALFTPYQHLEYAQELFSSEGRVHFAGEHTAFPHAWIETSMK 498
DB 602 TQGNRRCKWALDPLESASWASPTVQGHLYLPEYQTRNNLVFVGEHTSYTHAMIASALE 661
QY 499 SAIRAATNI 507
DB 662 SGIRGSVQL 670

RESULT 15
US-09-482-273-266
; Sequence 266, Application US/09482273
; Patent No. 6534631
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 71 Human Secreted Proteins
; FILE REFERENCE: P2030P1
; CURRENT APPLICATION NUMBER: US/09/482,273
; CURRENT FILING DATE: 2000-01-13
; EARLIER APPLICATION NUMBER: PCT/US99/15849
; EARLIER FILING DATE: 1999-07-14
; EARLIER APPLICATION NUMBER: 60/092,921
; EARLIER FILING DATE: 1998-07-15
; EARLIER APPLICATION NUMBER: 60/092,922
; EARLIER FILING DATE: 1998-07-15
; EARLIER APPLICATION NUMBER: 60/092,956
; EARLIER FILING DATE: 1998-07-15
; NUMBER OF SEQ ID NOS: 267
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 266
; LENGTH: 212
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (123)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-482-273-266

Query Match 14.3%; Score 387; DB 4; Length 212;
Best Local Similarity 46.9%; Pred. No. 2.7e-27;
Matches 84; Conservative 25; Mismatches 44; Indels 26; Gaps 6;

QY 341 EALRSVHYDSSTKILLTFRDKFWEDDGGIRGGKSITDGPSRYIYVPSHSFHTNETIGVLLA 400
DB 7 EALRLHYVPATKVFSLFRPFRFWEHIEGHSNTDRPSRMIFTP-----PPREGALLJA 61

Qy 401 SYTWSDESLFLGASDEELKELALRDLAKIHG---EQVWDKCTGVIVKKWSADPYSLGAF 457
| | | | : | | | | | | | : | | | | : | | | | : | | | |
Db 62 SYTWSDAAAAFAGLSREEALRLALDDVAALHGPVVRQLWDG-TGV-VKRWAEQHSQGGF 119
| | | | : | | | | | | | : | | | | : | | | | : | | | |
Qy 458 ALFTPYQHLEYAQELFSSE-----GRVHFAGEHTAPPHAWIETSMKSAIRAAATNIN 508
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Db 120 VVOXP-----ALWQTEKDDWTVPYGRIYFAGEHTAYPHGWVETAVKSAIRAAIKIN 170
| | | | : | | | | | | | : | | | | : | | | | : | | | |

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Job time : 45 secs

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OM protein - protein search, using sw model

Run on: October 4, 2005, 13:40:50 ; Search time 479 Seconds
(without alignments)
1277.735 Million cell updates/sec

Title: US-10-645-094-1

Perfect score: 2703

Sequence: 1 MNLHVVKWKLVSVLITLY.....TNINKVANEESTIETKDEL 524

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 6959266 seqs, 1168006243 residues

Total number of hits satisfying chosen parameters: 6959266

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 2: /cgn2_6/ptodata/1/paa/US06 COMB.pcp.*
- 3: /cgn2_6/ptodata/1/paa/US07 COMB.pcp.*
- 4: /cgn2_6/ptodata/1/paa/US08 COMB.pcp.*
- 5: /cgn2_6/ptodata/1/paa/US081 COMB.pcp.*
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- 37: /cgn2_6/ptodata/1/paa/US60 COMB.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	2703	100.0	524	32	US-10-644-142A-1	Sequence 1, Appli
3	2703	100.0	524	32	US-10-645-094-1	Sequence 1, Appli
4	1063.5	39.3	516	22	US-09-791-537-143961	Sequence 143961,
5	1059.5	39.2	516	22	US-09-791-537-131193	Sequence 131193,
6	1034	38.3	630	22	US-09-791-537-143903	Sequence 143903,
7	1034	38.3	630	24	US-09-938-795A-1	Sequence 1, Appli
8	999	37.0	567	1	PCT-US02-08123-1068	Sequence 1068, Ap
9	999	37.0	567	1	PCT-US02-08278-1025	Sequence 1025, Ap
10	999	37.0	567	1	PCT-US02-09785-590	Sequence 590, App
11	999	37.0	567	1	PCT-US03-21083-4	Sequence 4, Appli
12	999	37.0	567	23	US-09-882-636-13	Sequence 13, Appli
13	999	37.0	567	24	US-09-938-795A-2	Sequence 2, Appli
14	999	37.0	567	24	US-09-946-374-84	Sequence 84, Appli
15	999	37.0	567	26	US-10-001-054-24	Sequence 24, Appli
16	999	37.0	567	26	US-10-006-041A-84	Sequence 84, Appli
17	999	37.0	567	26	US-10-006-063A-84	Sequence 84, Appli
18	999	37.0	567	26	US-10-006-116A-84	Sequence 84, Appli
19	999	37.0	567	26	US-10-006-117A-84	Sequence 84, Appli
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41	999	37.0	567	26	US-10-012-252A-84	Sequence 84, Appli
42	999	37.0	567	26	US-10-012-253A-84	Sequence 84, Appli
43	999	37.0	567	26	US-10-012-754A-84	Sequence 84, Appli
44	999	37.0	567	26	US-10-012-755A-84	Sequence 84, Appli
45	999	37.0	567	26	US-10-013-430A-84	Sequence 84, Appli

ALIGNMENTS

RESULT 1
US-10-644-142-1
; Sequence 1, Application US/10644142
; GENERAL INFORMATION:
; APPLICANT: Iwamoto, Mitsunori; Jung, Sang-Kee
; TITLE OF INVENTION: NOVEL PROTEIN, ITS GENE, REAGENTS FOR INDUCING
; FILE OF INVENTION: APAPTOSIS, AND ANTICANCER AGENTS
; FILE REFERENCE: 4703/OF214
; CURRENT APPLICATION NUMBER: US/10/644,142
; CURRENT FILING DATE: 2003-08-20
; PRIOR APPLICATION NUMBER: US/09/230,388
; PRIOR FILING DATE: 1999-01-22
; PRIOR APPLICATION NUMBER: PCT/JP98/02361
; PRIOR FILING DATE: 1998-05-22
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 524
; TYPE: PRT

i		ORGANISM: Scomber japonicus	
US-10-644-142-1			
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Best Local Similarity		100.0%; Pred. No. 1.1e-246;	
Matches 524; Conservative		0; Mismatches 0; Indels 0; Gaps 0;	
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Db	1	MNLHVVKWKL SVSVSLITLYSHTVALSKLHKLADCLDKDYDTLLQTLQDGLPHINTSH	60
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Qy	121	H R I V Q M F V K K L G V E N N E F V M T D D N T F Y L V N G V R E T Y V V Q E N P D V L K Y N V S E S E K G I S A D	180
Db	121	H R I V Q M F V K K L G V E N N E F V M T D D N T F Y L V N G V R E T Y V V Q E N P D V L K Y N V S E S E K G I S A D	180
Qy	181	D L L D R A L Q K V K E E V A N G C K A A L E K Y D R Y S V K E Y L K E E G G L S P G A V R M I G D L L N E O S L M Y	240
Db	181	D L L D R A L Q K V K E E V A N G C K A A L E K Y D R Y S V K E Y L K E E G G L S P G A V R M I G D L L N E O S L M Y	240
Qy	241	T A L S E M I Y D Q A D V N D S V T Y H E V T G G S D L L P E A F L S V L D P I L L N S K V K H I R Q S D K G V I V S	300
Db	241	T A L S E M I Y D Q A D V N D S V T Y H E V T G G S D L L P E A F L S V L D P I L L N S K V K H I R Q S D K G V I V S	300
Qy	301	Y O T G N E S S L M D L S A D I V L V T T T A K A A L F I D F D P P L S I S K M E A L R S V H Y D S S T K I L L T F R D	360
Db	301	Y O T G N E S S L M D L S A D I V L V T T T A K A A L F I D F D P P L S I S K M E A L R S V H Y D S S T K I L L T F R D	360
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RESULT 3			
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; Sequence 1, Application US/10645094			
; GENERAL INFORMATION:			
; APPLICANT: Iwamoto, Mitsunori; Jung, Sang-kee			
; TITLE OF INVENTION: NOVEL PROTEIN, ITS GENE, REAGENTS FOR INDUCING			
; FILE REFERENCE: 4703/0F214			
; CURRENT APPLICATION NUMBER: US/10/645,094			
; PRIOR FILING DATE: 2003-08-21			
; PRIOR APPLICATION NUMBER: US/09/912,176			
; PRIOR FILING DATE: 2001-07-24			
; PRIOR APPLICATION NUMBER: US 09/230,388			
; PRIOR FILING DATE: 1999-01-22			
; PRIOR APPLICATION NUMBER: PCT/JP98/02261			
; PRIOR FILING DATE: 1998-05-22			
; NUMBER OF SEQ ID NOS: 2			
; SOFTWARE: PatentIn Ver. 2.0			
; SEQ ID NO 1			
; LENGTH: 524			
; TYPE: PRT			
; ORGANISM: Scomber japonicus			
US-10-645-094-1			
Query Match			
Best Local Similarity			
Matches 524; Conservative			
100.0%; Score 2703; DB 32; Length 524;			
Pred. No. 1.1e-246;			
Mismatches 0; Indels 0; Gaps 0;			
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Db	1	MNLHVVKWKL SVSVSLITLYSHTVALSKLHKLADCLDKDYDTLLQTLQDGLPHINTSH	60
Qy	61	HVVI V GAGMAGLTA A K L L Q D A G H T V T I L E A N D R V G R V E T Y R N E K E G W A E M G A M R I P S S	120
Db	61	HVVI V GAGMAGLTA A K L L Q D A G H T V T I L E A N D R V G R V E T Y R N E K E G W A E M G A M R I P S S	120
Qy	121	H R I V Q M F V K K L G V E N N E F V M T D D N T F Y L V N G V R E T Y V V Q E N P D V L K Y N V S E S E K G I S A D	180
Db	121	H R I V Q M F V K K L G V E N N E F V M T D D N T F Y L V N G V R E T Y V V Q E N P D V L K Y N V S E S E K G I S A D	180

Qy	181	DLLDRLAQKVKEVEANGKAALEKYDYRYSVKEYLKEEGLSPGAVRMIGDLLNEQSLMY	240
Db	181		
	181	DLLDRLAQKVKEVEANGKAALEKYDYRYSVKEYLKEEGLSPGAVRMIGDLLNEQSLMY	240
Qy	241	TALSEMIYDQADVNSVTYHEVTGGSDLLPEAFLSVLDPILLNSVKVHIROSDKGVIVS	300
Db	241		
	241	TALSEMIYDQADVNSVTYHEVTGGSDLLPEAFLSVLDPILLNSVKVHIROSDKGVIVS	300
Qy	301	YQTGNESIMDLASDIVLVTTTAKAALFTDFDPPPLISIKWEALRSVHYVDSSFKILLTFRD	360
Db	301		
	301	YQTGNESIMDLASDIVLVTTTAKAALFTDFDPPPLISIKWEALRSVHYVDSSFKILLTFRD	360
Qy	361	KFWEDDGIRGGKSITDGPFSRYIYPFSPHSFHTNETICVLLASYTSWDSLELLFGASDEELK	420
Db	361		
	361	KFWEDDGIRGGKSITDGPFSRYIYPFSPHSFHTNETICVLLASYTSWDSLELLFGASDEELK	420
Qy	421	ELALRLDLAKIHGEQVMDKCTGVIVKWSADPSYSLGAFALFTPQYHLEYAQELFSSEGRVH	480
Db	421		
	421	ELALRLDLAKIHGEQVMDKCTGVIVKWSADPSYSLGAFALFTPQYHLEYAQELFSSEGRVH	480
Qy	481	FAGEHTAPPHAWIETSMKSAPRAATNINKVANEESTIEHTKOEL	524
Db	481		
	481	FAGEHTAPPHAWIETSMKSAPRAATNINKVANEESTIEHTKOEL	524

```

RESULT 4
US-09-791-537-143961
; Sequence 143961, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBERS
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791.537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 151055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 143961
; LENGTH: 516
; TYPE: PRT
; ORGANISM: Crotalus atrox
US-09-791-537-143961

```

Query Match 39.3%; Score 1063.5; DB 22; Length 516;
Best Local Similarity 44.0%; Pred. No. 6e-91;
Matches 218; Conservative 96; Mismatches 169; Indels 13; Gaps 7

Qy	33	LADCLEDKDYDTLLQTLDNGLPHINTSHHVIVVGAGMAGLTAACKLQDAGHTVTVILEAND	92
Db	25	LEECFRETDYBEFLIAKNGLTATSNPKRVIVVGAGMAGLSAAVYVLAGAGHQVTVLEASE	84
	93	RVGGRVETRYNEKEGWAEMGAMRI PSSHRIVQVFKVLGVEMNEFVMTDONTFYLVNGV	152
Db	85	RVGGRVTRYR--KKDWANLGPMLPTKHRIVREYIKKFDLKLNEFSQENENAWFYIKNI	142
Qy	153	RERTYVVOENPDVLKYNVSEBKGISADDDLLDRALQKVKEVEANGCKAAALEKYDRISVK	212
Db	143	RKRVRVKNPGLUEYVPKSEEGKSAQLVYESLRKVKVLEKRTNCKYILDKYDVTYSTK	202
Qy	213	EYLKEEGGLSPGAVRMIGDILLNEQSLMYTALSEMIYQDQVNDVSYVHVEVTGGSDLLPEA	272
Db	203	EYLLKEGNLSPGAVDMIGDILLNEDSGYVVSFIESLKHDDIFGYEKRPDEIVGCHMDQLPTS	262
Qy	273	FLSVL--DVPILNSKVKHIRQSDKGVIVSYQT--GNESSLMDLSADIVLVTTTAKAALFI	329
Db	263	MYEAIKEKVQVHFNAFVIEIQONDREATVTVYQTSANEMS--SVTADVIVICTTSRAARRI	320
Qy	330	DPDPPLSISKWEALRSVHYDSSTKILLITFRDKFWEDDGIRCGKGIITGDPSPRIYYPHSF	389
Db	321	KFEPPLPPKAAHALRSVHYRSGTKIFUTCKKKPWEDDGIRCGKSTTDLPSRFIYYPHNF	380

```

QY      390 HTNETIGVLLASYTWSDESLFLGASDEELKELALRDIAKH- --GEQVWDKCTGVIVKK   446
D8      TSG--VGVIIA-YGIGDDANFQALDFKDCADIVINDLSLIHQLPKEDIQTFCRPSMIQR   437
QY      447 WSPDPYSLGAFALTPTPYQHLYEYAQBELFSSEGRVHFAGBHTAPPHAWIETMSKAIRAATN   506
D8      438 WSLDKYAMGGITTTTPYQOHFSEALTAPPFKRIYEPAGEYTAQFHGWIDSTIKSGLTAAARD   497
QY      507 INKVANEESTIEHTKD 522
D8      498 VNRAENPFGIHLSND 513

RESULT 5
US-09-791-537-131193
; Sequence 131193, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND PA
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 131193
; LENGTH: 516
; TYPE: PRT
; ORGANISM: Crotalus adamanteus
US-09-791-537-131193
```

Query Match 39.2%; Score 1059.5; DB 22; Length 516;
Best Local Similarity 44.0%; Pred. NO. 1.4e-90;
Matches 218; Conservative 94; Mismatches 171; Indels 13; Gaps 7

Qy	33	LABCLEDKOYDTLLQTLNDLNGPLHPTNTHSHVVIVGAGMAGLTAAKLQDAGHTVTVILEAND	92
Db	25	LEBCFRETDOEEFLAEIAKGLTATSNPKRVIVIVGAGMAGLSAAVVLACAGHQTVLEASE	84
Qy	93	RVGGRVETRYNEKEGWYAENGAMRIPSSHRIWQHFVKVLGVEMHEFVMTDDNTFFLVNGV	152
Db	85	RVGGRVRTYR--KDWYANILGPMLPTKHRIVREYIKFKDLKLNFEFSQENENAWFYIKNI	142
Qy	153	RERTYVVOENPDVLKNVSESEKGISADLLDLRALOKVBEVEANGCKAALKKYDRYSVK	212
Db	143	RKRVRKVNNPGGLEVPVKFSEBKSAAQLVRESLRKVVELSRNCKYYILLDKDYDTSTK	202
Qy	213	EYLKEBGSLSPGARVMIGDILLNQSLMYTALSEMIYQADVNDSVTYHEVTGGSDLLPEA	272
Db	203	EYLLKEGNLSPGAVDMIGDLLNEDSGYVVSPIESLKHDDIFGYEKRPDEIVGMWDLPTS	262
Qy	273	FLSVL--DVPIILNSKHVIRQSKGVIVSYQT-GNESSLMDSLADIVLVTTTAKAALFI	329
Db	263	MYEAIKEKVQHFNARVIEIQONDREATVYTQSANEWS--SVTADYVIVCTTSRAARRI	320
Qy	330	DFDPPLSISKWEALRSVHYDSSTKILLTFPRDKFWEDDGIRCGKIITGPSRYIIYPHSHF	389
Db	321	KFEPPLPPKAHALRSVHYRSGTKIFLCTCKFWEDDGIHGKSTTDLPSRFIYYPHNHF	380
Qy	390	HTNETTIGVLLASTWSEDSELFLGASDEELKELALRDLAETH---GEQVMDKCTGVIVKK	446
Db	381	TSG--YGVIIA-YGIGDANFFQALDPKCADIVINDLSLIHELPKEDIOQTFCHPSMTQR	437
Qy	447	WSADPYSLGAFALFTPYQHLEYAQELFPSSSEGRVHFACEHTAFPRAWIETSMKSARAATTN	506
Db	438	WSLDKYAMGIIITFTPYQHPFSEALTAPKRYIFAGEYTAQPFHWIDSTIKSGILTAARD	497
Qy	507	INKVANEESTIEHTKD	522
Db	498	VNRASENPSPGIHLNSD	513

RESULT 6

US-09-791-537-143903

; Sequence 143903, Application US/09791537

; GENERAL INFORMATION:

; APPLICANT: Bionomix, Inc.

; APPLICANT: Debe, Derek

; APPLICANT: Danzer, Joseph

; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE

; FILE REFERENCE: 261/210

; CURRENT APPLICATION NUMBER: US/09/791,537

; CURRENT FILING DATE: 2001-02-22

; NUMBER OF SEQ ID NOS: 153055

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 143903

; LENGTH: 630

; TYPE: PRT

; ORGANISM: Mus musculus

US-09-791-537-143903

Query Match 38.3%; Score 1034; DB 22; Length 630;

Best Local Similarity 43.5%; Pred. No. 5.3e-88;

Matches 212; Conservative 100; Mismatches 163; Indels 12; Gaps 6;

```
QY 26 ALSLKEHLADCLDEDKDYDTLLQTLDNGLPHINTSHHVIVVGVAGMAGLTAAKLLQDAGHTV 85
DB 25 AASSLNPIEKCMEDHDYEQLLKVVTLGLNRTSKPKQVWVGVAGVAGLVAAMKLSDAGHKV 84
QY 86 TLEANDRVGGRVETRYNEKEGVAEMGAMRIPSSHRIVQWFKVLGVEMNEFVMTDDNT 145
DB 85 TLEADNRIGRIFFRDEKGTWIGELGAMRMPSSHRILHLKLCRTLGLNLTOFTQYDENT 144
QY 146 FYLVNGVRERTYVVOENPDVLKYNVSESEKISADLLDRALQKVKEEVEANGCKAALEK 205
DB 145 WTEVHNVKLRNVVVEKMPKELGYNLNNRERGHSPEDIYQMALNKAFAKDKALGCKKAMNK 204
QY 206 YDRYSVKEYLKEEGLSPGAVRMIGDLLNEQSLMYTALSEMIYDOADVNDSVTYHEVTGG 265
DB 205 FNKHTLLEYLLEEGNLSRPVQLLDGVNMESEGFYLSFAEALRAHACLSDRURYRIVGG 264
QY 266 SDLLPEAFSLVDVPIILNSKVKHIRQSDKGIVISYQTNESLSMDLSADIVLVTTTAKA 325
DB 265 WDLPLRALLSLSGALLNAPVVSITQGRNDRVHIATSLHSE-KTLTADVVLTLTASGPA 323
QY 326 ALFIDPDPPLSLSKMEALRSVHYDSSTKILLTFRDKFWEDDGIKGGKISITDGPRIYIYP 385
DB 324 LQRITFSPPLTRKQREALRALHYVAASKVFLSFRPFWHEEHIEGGHSNTDRPSRLIFYP 383
QY 386 SHSFHTNETIGVLLASYTWSDESLLFLGASDEELKELALRDLAKTHGE--QVWDKCTGV 442
DB 384 ARGECS-----LLLASVTWSDAAAPFAGLSTQDTLRVLQDVVAALHGPVFRMLWDG-RGV 437
QY 443 IVKWSADPYSLGAFALFTPYQHLEYAQELFSSSE-GRVHFAGEHTAFPHAMTSMKSAI 501
DB 438 -VKRWAEDPHSQGGFVQPPPLYGREADYDWSAPFGRIYFAGEHTALPHGWVETAVKSGL 496
QY 502 RAATNIN 508
DB 497 RAAVRIN 503
```

RESULT 7

US-09-938-795A-1

; Sequence 1, Application US/09938795A

; GENERAL INFORMATION:

; APPLICANT: CHU, CHARLES CHIYUAN

; APPLICANT: CHAVAN, SANGEETA S.

; APPLICANT: MASON, JAMES M.

; TITLE OF INVENTION: HUMAN INTERLEUKIN-FOUR INDUCED PROTEIN

; FILE REFERENCE: LIJ-9000-US

; CURRENT APPLICATION NUMBER: US/09/938,795A

```
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: 60/227,818
; PRIOR FILING DATE: 2000-08-25
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 630
; TYPE: PRT
; ORGANISM: Mus sp.
US-09-938-795A-1
```

```
Query Match 38.3%; Score 1034; DB 24; Length 630;
Best Local Similarity 43.5%; Pred. No. 5.3e-88;
Matches 212; Conservative 100; Mismatches 163; Indels 12; Gaps 6;
```

```
QY 26 ALSLKEHLADCLDEDKDYDTLLQTLDNGLPHINTSHHVIVVGVAGMAGLTAAKLLQDAGHTV 85
DB 25 AASSLNPIEKCMEDHDYEQLLKVVTLGLNRTSKPKQVWVGVAGVAGLVAAMKLSDAGHKV 84
QY 86 TLEANDRVGGRVETRYNEKEGVAEMGAMRIPSSHRIVQWFKVLGVEMNEFVMTDDNT 145
DB 85 TLEADNRIGRIFFRDEKGTWIGELGAMRMPSSHRILHLKLCRTLGLNLTOFTQYDENT 144
QY 146 FYLVNGVRERTYVVOENPDVLKYNVSESEKISADLLDRALQKVKEEVEANGCKAALEK 205
DB 145 WTEVHNVKLRNVVVEKMPKELGYNLNNRERGHSPEDIYQMALNKAFAKDKALGCKKAMNK 204
QY 206 YDRYSVKEYLKEEGLSPGAVRMIGDLLNEQSLMYTALSEMIYDOADVNDSVTYHEVTGG 265
DB 205 FNKHTLLEYLLEEGNLSRPVQLLDGVNMESEGFYLSFAEALRAHACLSDRURYRIVGG 264
QY 266 SDLLPEAFSLVDVPIILNSKVKHIRQSDKGIVISYQTNESLSMDLSADIVLVTTTAKA 325
DB 265 WDLPLRALLSLSGALLNAPVVSITQGRNDRVHIATSLHSE-KTLTADVVLTLTASGPA 323
QY 326 ALFIDPDPPLSLSKMEALRSVHYDSSTKILLTFRDKFWEDDGIKGGKISITDGPRIYIYP 385
DB 324 LQRITFSPPLTRKQREALRALHYVAASKVFLSFRPFWHEEHIEGGHSNTDRPSRLIFYP 383
QY 386 SHSFHTNETIGVLLASYTWSDESLLFLGASDEELKELALRDLAKTHGE--QVWDKCTGV 442
DB 384 ARGECS-----LLLASVTWSDAAAPFAGLSTQDTLRVLQDVVAALHGPVFRMLWDG-RGV 437
QY 443 IVKWSADPYSLGAFALFTPYQHLEYAQELFSSSE-GRVHFAGEHTAFPHAMTSMKSAI 501
DB 438 -VKRWAEDPHSQGGFVQPPPLYGREADYDWSAPFGRIYFAGEHTALPHGWVETAVKSGL 496
QY 502 RAATNIN 508
DB 497 RAAVRIN 503
```

RESULT 8

PCT-US02-08123-1068

; Sequence 1068, Application PC/TUS0208123

; GENERAL INFORMATION:

; APPLICANT: Human Genome Sciences, Inc.

; TITLE OF INVENTION: Human Secreted Proteins

; FILE REFERENCE: PS904PCT

; CURRENT APPLICATION NUMBER: PCT/US02/08123

; CURRENT FILING DATE: 2002-03-19

; PRIOR APPLICATION NUMBER: US 60/331,287

; PRIOR FILING DATE: 2001-11-13

; PRIOR APPLICATION NUMBER: US 60/306,171

; PRIOR FILING DATE: 2001-07-19

; PRIOR APPLICATION NUMBER: US 60/277,340

; PRIOR FILING DATE: 2001-03-21

; NUMBER OF SEQ ID NOS: 2048

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 1068

; LENGTH: 567

; TYPE: PRT

; ORGANISM: Homo sapiens


```
QY 182 LLDRALQKVEEVEANGKAALKEKYDRYSVKEYLKEEGLSPGAVRMIGDLNQLMYT 241
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 182 IQMALNQALKDLKALGCRKAMKFERHTLLEYLLGEGNLSRPAVQLLGDVMSDGPFL 241
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 242 ALSEMIYQADVNDVTHVETGSGDLLPEAPFLSVLDVPILLNSKVKHROSQKGVIVSY 301
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 242 SFAEALRAHSCLSRLQYSRIVGGWDLPLPRALLSSLSGLVLLNAPVAVMTQPHDVHVO 301
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 302 QTGNES-SLMDLSADIVLVTAKAALFIDPDPPLSISKMEALRSVHYDSSTKILLTRFD 360
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 302 ETSPPARNLKVLKADVLLTASGPAVKRITSPPLPRHMQEALRLHVTYPATKVPFLSPRR 361
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 361 KFWEDDGIRGKSIITDGPFSRYIYYPSSHFTNETIGVLLASYTWSDESLLFLGASDEBLK 420
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 362 PFWREEHIEGHSNTDRPSRMIFYP-----PPREGALLASYTWSDAAAAFAGLSREAL 416
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 421 ELALRDLAKING-----EQWMDKCTGVIVKWSADPYSLGAPALFTPYQHLEYVAQELFSSE- 476
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 417 RLALDDVAALGHPVVRQLWDG-TGV-VKRWAEDQHSQGGFVVQPP-----ALWQTEK 466
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 477 -----GRVHPAGHTAPPHAWIETSMKSAIRAATNIN 508
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 467 DDWTVPGRIYPAGEHTAYPHGWVETAVKSALRAAIKIN 505
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
```

```
RESULT 11
PCT-US03-21083-4
; Sequence 4, Application PC/TUS0321083
; GENERAL INFORMATION:
; APPLICANT: GENENTECH, INC.
; APPLICANT: HENRY CHIU
; APPLICANT: HILARY CLARK
; APPLICANT: KATHRYN DENNIS
; APPLICANT: SHERMAN FONG
; APPLICANT: JILL SCHOENFELD
; APPLICANT: WILLIAM WOOD
; APPLICANT: THOMAS WU
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TREATMENT OF IMMUNE
; FILE REFERENCE: P1973R1-PCT
; CURRENT APPLICATION NUMBER: PCT/US03/21083
; PRIOR FILING DATE: 2003-07-08
; PRIOR APPLICATION NUMBER: US 60/394,485
; PRIOR FILING DATE: 2002-07-08
; NUMBER OF SEQ ID NOS: 28
; SEQ ID NO 4
; LENGTH: 567
; TYPE: PRT
; ORGANISM: Homo sapien
PCT-US03-21083-4
```

```
Query Match 37.0%; Score 999; DB 1; Length 567;
Best Local Similarity 41.8%; Pred. No. 9.3e-85;
Matches 217; Conservative 99; Mismatches 171; Indels 32; Gaps 9;

QY 3 LHVWKLSVSVSLITLYSHT-VALSLKEHLADCLEDKDYDTLLQTLNDGLPHINTSHH 61
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 6 LHL-----LVLPILLSVASQDKAERSQDPFKCMQDPVEQLLKVVWTGVLNRLTKPQR 61
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 62 VVIVGAGMAGLTAALKLODAGHTVILBANDRVGRVETRYNEKEGWAENGAMRIPSSH 121
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 62 VVIVGAGVAGLVAARKVLSGAGHKVITLADNRIGRIFTYRDQNTGTIGELGAMRMPSSH 121
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 122 RIVQFVKLVGMENFEVMTDDTPLYNGVRERYVYQENPDVLKYNVSESEKISADD 181
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 122 RILHLKCOGLGULNLTFTQYDKNTWTVEHVKLRNVYVEKPEKLYGALRPOEKGHSHPD 181
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 182 LLDRALQKVEEVEANGKAALKEKYDRYSVKEYLKEEGLSPGAVRMIGDLNQLMYT 241
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 182 IQMALNQALKDLKALGCRKAMKFERHTLLEYLLGEGNLSRPAVQLLGDVMSDGPFL 241
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 242 ALSEMIYQADVNDVTHVETGSGDLLPEAPFLSVLDVPILLNSKVKHROSQKGVIVSY 301
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
```

```
Db 242 SFAEALRAHSCLSRLQYSRIVGGWDLPLPRALLSSLSGLVLLNAPVAVMTQPHDVHVO 301
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 302 QTGNES-SLMDLSADIVLVTAKAALFIDPDPPLSISKMEALRSVHYDSSTKILLTRFD 360
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 302 ETSPPARNLKVLKADVLLTASGPAVKRITSPPLPRHMQEALRLHVTYPATKVPFLSPRR 361
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 361 KFWEDDGIRGKSIITDGPFSRYIYYPSSHFTNETIGVLLASYTWSDESLLFLGASDEBLK 420
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 362 PFWREEHIEGHSNTDRPSRMIFYP-----PPREGALLASYTWSDAAAAFAGLSREAL 416
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 421 ELALRDLAKING-----EQWMDKCTGVIVKWSADPYSLGAPALFTPYQHLEYVAQELFSSE- 476
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 417 RLALDDVAALGHPVVRQLWDG-TGV-VKRWAEDQHSQGGFVVQPP-----ALWQTEK 466
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 477 -----GRVHPAGHTAPPHAWIETSMKSAIRAATNIN 508
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 467 DDWTVPGRIYPAGEHTAYPHGWVETAVKSALRAAIKIN 505
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
```

```
RESULT 12
US-09-882-636-13
; Sequence 13, Application US/09882636
; GENERAL INFORMATION:
; APPLICANT: Botstein, David
; APPLICANT: Goddard, Audrey
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth
; APPLICANT: Lawrence, David, A
; APPLICANT: Roy, Margaret, Ann
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TREATMENT OF TUMOR
; FILE REFERENCE: P2509R1C1
; CURRENT APPLICATION NUMBER: US/09/882,636
; CURRENT FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: 60/113,296
; PRIOR FILING DATE: December 22, 1998
; PRIOR APPLICATION NUMBER: 60/112,850
; PRIOR FILING DATE: December 16, 1998
; PRIOR APPLICATION NUMBER: 60/107,783
; PRIOR FILING DATE: November 10, 1998
; PRIOR APPLICATION NUMBER: 60/088,742
; PRIOR FILING DATE: June 10, 1998
; PRIOR APPLICATION NUMBER: 60/086,414
; PRIOR FILING DATE: May 22, 1998
; PRIOR APPLICATION NUMBER: 60/083,500
; PRIOR FILING DATE: April 29, 1998
; PRIOR APPLICATION NUMBER: 60/082,767
; PRIOR FILING DATE: April 23, 1998
; PRIOR APPLICATION NUMBER: 60/074,086
; PRIOR FILING DATE: February 9, 1998
; PRIOR APPLICATION NUMBER: 60/070,440
; PRIOR FILING DATE: January 5, 1998
; PRIOR APPLICATION NUMBER: 60/069,873
; PRIOR FILING DATE: December 17, 1997
; PRIOR APPLICATION NUMBER: 60/069,702
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,694
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,696
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/066,772
; PRIOR FILING DATE: November 24, 1997
; PRIOR APPLICATION NUMBER: 60/032,705
; PRIOR FILING DATE: December 12, 1996
; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: December 1, 2000
; PRIOR APPLICATION NUMBER: 09/709,238
; PRIOR FILING DATE: November 8, 2000
; PRIOR APPLICATION NUMBER: 09/664,610
; PRIOR FILING DATE: September 18, 2000
; PRIOR APPLICATION NUMBER: 09/665,350
; PRIOR FILING DATE: September 18, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/23522
```



```
QY 3 LHVWKLSVSVLITLYSHT-VALSLKEHLADCLEDKDYTLQTLQDGLPHINTSHH 61
; PRIOR APPLICATION NUMBER: 60/098750
; PRIOR FILING DATE: 1998-09-01
Db 6 LHL-----LVLPILLSVASQDWKERSQDPPEKCMQDPDYEQLLKLVTVWGLNRTLKQOR 61
; PRIOR APPLICATION NUMBER: 60/098803
; PRIOR FILING DATE: 1998-09-02
QY 62 VVIVGAGMAGLTAALKLODAGHTVITLEANDRVGGRVETRYNEKEGVAEMGAMRIPSSH 121
; PRIOR APPLICATION NUMBER: 60/098821
; PRIOR FILING DATE: 1998-09-02
Db 62 VIVGAGVAGLVAALKVLSAGCHKVITLEADNRIGGRIFTYRDONTGWIGELGAMRMPSSH 121
; PRIOR APPLICATION NUMBER: 60/098843
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QY 122 RIVQFVKVLGVEMNEFVMTDNTFYLYNGVPRYVQENPDVLKYNVSESEKISADD 181
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; PRIOR FILING DATE: 1998-09-09
Db 122 RIHLKLCQGLGJNLTKFTQYDKNTWTEVHEVKLRNVVVEKPEKLGALRPQEKHSPED 181
; PRIOR APPLICATION NUMBER: 60/099596
; PRIOR FILING DATE: 1998-09-09
QY 182 LLDRLAQKQKBEVEANGKAALEKDYKSVKEYLKEEGLSPGAVRMIGDLINQOSLMYT 241
; PRIOR APPLICATION NUMBER: 60/099602
; PRIOR FILING DATE: 1998-09-09
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; PRIOR APPLICATION NUMBER: 60/099642
; PRIOR FILING DATE: 1998-09-09
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; PRIOR APPLICATION NUMBER: 60/099741
; PRIOR FILING DATE: 1998-09-10
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; PRIOR FILING DATE: 1998-09-10
QY 302 QTGNES-SLMDLSADIVLVTTAKAALFIDFDPPLSISKMEALRSVHYDSSTKILLTERD 360
; PRIOR APPLICATION NUMBER: 60/099763
; PRIOR FILING DATE: 1998-09-10
Db 302 ETSPARNLKVLUADVLLTASGPAVKRITFSPPLRHMQEARLRLHYVPATKVFLSRR 361
; PRIOR APPLICATION NUMBER: 60/099792
; PRIOR FILING DATE: 1998-09-10
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; PRIOR APPLICATION NUMBER: 60/099808
; PRIOR FILING DATE: 1998-09-10
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; PRIOR APPLICATION NUMBER: 60/099812
; PRIOR FILING DATE: 1998-09-10
QY 421 ELALRDLAKIHG---EQWMDKCTGVIVKWSADPYSLGAFALFTPYOHLVYAQELFSSE- 476
; PRIOR APPLICATION NUMBER: 60/099815
; PRIOR FILING DATE: 1998-09-10
Db 417 RLALDDVAALHGVVVRQLWDG-TGV-VKRWADQHSQGVVQVP-----ALWQTEK 466
; PRIOR APPLICATION NUMBER: 60/099816
; PRIOR FILING DATE: 1998-09-10
QY 477 -----GRVHFAGHTAPPHAWIETSMKSATRAATNN 508
; PRIOR APPLICATION NUMBER: 60/100385
; PRIOR FILING DATE: 1998-09-15
Db 467 DDMTPVYGRYFAGEHTAYPHGWVETAVKSAURAAIKIN 505
; PRIOR APPLICATION NUMBER: 60/100388
; PRIOR FILING DATE: 1998-09-15
RESULT 14
US-09-946-374-84
; Sequence 84, Application US/09946374
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C1
; CURRENT APPLICATION NUMBER: US/09/946,374
; CURRENT FILING DATE: 2001-09-04
; PRIOR APPLICATION NUMBER: 60/098716
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098723
; PRIOR FILING DATE: 1998-09-01
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; PRIOR FILING DATE: 1998-09-01
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; PRIOR FILING DATE: 1998-10-26
; PRIOR APPLICATION NUMBER: 60/105807
; PRIOR FILING DATE: 1998-10-27
; Query Match 37.0%; Score 999; DB 24; Length 567;
; Best Local Similarity 41.8%; Pred. No. 9.3e-85;
; Matches 217; Conservative 99; Mismatches 171; Indels 32; Gaps 9;
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Db 6 LHL-----LVLVPILLSLVASODWKAERSODPEKCMQDPDYEQLLKVVWTWGLNRLTKPQR 61
QY 62 VVIVGAGMAGLTAAKLLQDAGHTVILEANDVGVGRVETYNKEKGWYAEAMGAMRTPSSH 121
Db 62 VIVVGAGVAGLVAARKVLS DAGHKVLTILBADRNRIGRIFTRDQNTGWI GELGAMRMPSSH 121
QY 122 RIVQWFKVLGVENNEFVMTDDNTFYLVNGVRETYVVVOENPDVLKYNVSESEKGISADD 181
Db 122 RILHKLCOGLNLTKFTQYDKNTWTEVHEVKLRNVYVEKVPKLGVALRPOEKGHSPED 181
QY 182 LLDRALQKVBEVEANGCKAALKEKYDRYSVREYLKEEGSLSPGAVRMIGDLLNEQSLMYT 241
Db 182 IYQVAMALQALKDLKALGCRKAMKFERHTLLEYLLGEGNLSRPAVQLLGDVMSDGFYV 241
QY 242 ALSEMIYDQADVNDVSVTYHEVTGGSDLLPEAPLSVLDVPILLNSKVGHIRQSDKGIVSY 301
Db 242 SFAEALRAHSCLSRLQYSRIVGGWDLPLRALLSSLSGLVLILNAPVAVMTQGPDHVQI 301
QY 302 QTGNES-SLMDLSADIVLTTAKAALFIDPPLLSISKMEALRSVHYVDSSTKILLTRPD 360
Db 302 ETSPPARNLKVLDVLLTASGPAVKRITPSPPLRHMQEARLRLHLYVPAVKVFLSPFR 361
QY 361 KFWEDDGI RGGKSI TDGSPRYIYPSHSHFHTNETIGVLLASYTWSDESLLFLGASDEELK 420
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QY 421 ELALRDLAKING---EQWMDKCTGVIVKWSADPYSLGAFALFTPYQHLEYAQELFSSP- 476
Db 417 RLALDDVAALHGPVVRQLWDG-TGV-VKRWAEQHSQGGFVVQPP-----ALWQTEK 466
QY 477 -----CRVHFACEHTAPPAWETSMSAIRAATNIN 508
Db 467 DDWTVPGRIYPAGEHTAYPHGWVETAVKLSALRAAIKIN 505

RESULT 15
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; Sequence 24, Application US/10001054
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Baker, Kevin
; APPLICANT: Goddard, Audrey
; APPLICANT: Gurney, Austin
; APPLICANT: Hebert, Carolyn
; APPLICANT: Henzel, William
; APPLICANT: Kabakoff, Rhona

APPLICANT: Shelton,David
APPLICANT: Smith,Victoria
APPLICANT: Watanabe,Colin
APPLICANT: Wood,William
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITING NEOPLASTIC
FILE REFERENCE: P3034R1PCT
CURRENT APPLICATION NUMBER: US/10/001,054
CURRENT FILING DATE: 2001-11-30
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PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/079689
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; PRIOR FILING DATE: 2001-06-20
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; PRIOR APPLICATION NUMBER: PCT/US01/21735
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: PCT/US01/27099
; PRIOR FILING DATE: 2001-08-29
; NUMBER OF SEQ ID NOS: 91
; SEQ ID NO 24
; LENGTH: 567
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-001-054-24

Query Match      37.0%; Score 999; DB 26; Length 567;
Best Local Similarity 41.8%; Pred. No. 9.3e-85;
Matches 217; Conservative 99; Mismatches 171; Indels 32; Gaps 9;

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Db      6 LHL-----LVLVPILLSVASQDWKAEBSQDPPEKCMQDPDYEQLLKVVVTWGLNRTLKPQR 61

Qy      62 VVIVGAGMAGLTAAKLLODAGHTVTILEANDRVGGRVETRYNEKEGWYAEMGAMRIPSSH 121
Db      62 VVIVGAGVAGLVAAKVLSGAGHKVTILEADNRIGGRIFTYRDQNTGWI GELGAMRMPSSH 121

Qy      122 RIVQWFKVLGVEMNEFVMTDDNTFYLVNGVRERTYVQENPDVLKYNVSESEKGISADD 181
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Qy      182 LLDRALQKVEVEANGCKAALKYDRYSVKEYLKEBGLSPGAVRMIGDLLNEOSLMYT 241
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Qy      302 QTGNES-SIMDLISADIVLTTTAKAALFIDFDPPLISIKMEALRSVHYDSSTKILLTERD 360
Db      302 ETSPPARNLVKADVLLTAGSPAVKRTFTSPPLPRHQEALRELHYVPATKVFLSFR 361

Qy      361 KPWEDDGRGKSIITDGRSRIYYPSHSHFNHNETIGVLLASYTWSDESLLFLGASDEELK 420
Db      362 PFWREEHIEGGHSNTRPSRMIFYP-----PPREGALLIASYTSDAFAAGLSREAL 416
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Qy      477 -----GRVHPAGEHTAPPHAWIETSMKSAIRAATNIN 508
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 4, 2005, 13:56:21 ; Search time 168 Seconds
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Title: US-10-645-094-1

Perfect score: 2703

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Searched: 1846076 seqs, 415116000 residues

Total number of hits satisfying chosen parameters: 1846076

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Post-processing: Minimum Match 0%

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- 22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2703	100.0	524	9	US-09-912-176-1
2	2703	100.0	524	15	US-10-644-142-1
3	2703	100.0	524	18	US-10-645-094-1
4	1034	38.3	630	10	US-09-938-795A-1
5	999	37.0	567	10	US-09-938-795A-2
6	999	37.0	567	10	US-09-946-374-84
7	999	37.0	567	13	US-10-001-054-24
8	999	37.0	567	13	US-10-053-107-2
9	999	37.0	567	14	US-10-028-072-476
10	999	37.0	567	14	US-10-140-808-476
11	999	37.0	567	14	US-10-121-049-476

12	999	37.0	567	14	US-10-123-904-476	Sequence 476, App
13	999	37.0	567	14	US-10-140-470-476	Sequence 476, App
14	999	37.0	567	14	US-10-175-746-476	Sequence 476, App
15	999	37.0	567	14	US-10-176-918-476	Sequence 476, App
16	999	37.0	567	14	US-10-176-921-476	Sequence 476, App
17	999	37.0	567	14	US-10-137-865-476	Sequence 476, App
18	999	37.0	567	14	US-10-140-474-476	Sequence 476, App
19	999	37.0	567	14	US-10-142-431-476	Sequence 476, App
20	999	37.0	567	14	US-10-143-114-476	Sequence 476, App
21	999	37.0	567	14	US-10-006-856A-84	Sequence 84, Appl
22	999	37.0	567	14	US-10-142-419-476	Sequence 476, App
23	999	37.0	567	14	US-10-123-262-476	Sequence 476, App
24	999	37.0	567	14	US-10-142-423-476	Sequence 476, App
25	999	37.0	567	14	US-10-006-818A-84	Sequence 84, Appl
26	999	37.0	567	14	US-10-121-050-476	Sequence 476, App
27	999	37.0	567	14	US-10-141-755-476	Sequence 476, App
28	999	37.0	567	14	US-10-213-145-2	Sequence 2, Appl
29	999	37.0	567	14	US-10-143-032-476	Sequence 476, App
30	999	37.0	567	14	US-10-006-485A-84	Sequence 84, Appl
31	999	37.0	567	14	US-10-013-907A-84	Sequence 84, Appl
32	999	37.0	567	14	US-10-015-499A-84	Sequence 84, Appl
33	999	37.0	567	14	US-10-123-108-476	Sequence 476, App
34	999	37.0	567	14	US-10-123-236-476	Sequence 476, App
35	999	37.0	567	14	US-10-123-261-476	Sequence 476, App
36	999	37.0	567	14	US-10-140-921-476	Sequence 476, App
37	999	37.0	567	14	US-10-140-928-476	Sequence 476, App
38	999	37.0	567	14	US-10-015-193A-84	Sequence 84, Appl
39	999	37.0	567	14	US-10-015-869A-84	Sequence 84, Appl
40	999	37.0	567	14	US-10-121-045-476	Sequence 476, App
41	999	37.0	567	14	US-10-123-292-476	Sequence 476, App
42	999	37.0	567	14	US-10-123-903-476	Sequence 476, App
43	999	37.0	567	14	US-10-124-819-476	Sequence 476, App
44	999	37.0	567	14	US-10-124-822-476	Sequence 476, App
45	999	37.0	567	14	US-10-140-925-476	Sequence 476, App

ALIGNMENTS

RESULT 1
US-09-912-176-1
; Sequence 1, Application US/09912176
; Patent No. US20020034804A1
; GENERAL INFORMATION:
; APPLICANT: Iwamoto, Mitsunori; Jung, Sang-Kea
; TITLE OF INVENTION: NOVEL PROTEIN, ITS GENE, REAGENTS FOR INDUCING
; FILE REFERENCE: 4703/OF214
; CURRENT APPLICATION NUMBER: US/09/912,176
; CURRENT FILING DATE: 2001-07-24
; PRIOR FILING DATE: 2001/07/24
; PRIOR APPLICATION NUMBER: US 09/230,388
; PRIOR FILING DATE: 1999-01-22
; PRIOR APPLICATION NUMBER: PCT/JF98/02261
; PRIOR FILING DATE: 1998-05-22
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 524
; TYPE: PRT
; ORGANISM: Scomber japonicus
US-09-912-176-1

Query Match 100.0%; Score 2703; DB 9; Length 524;
Best Local Similarity 100.0%; Pred. No. 1.3e-216;
Matches 524; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 MNLHVWKLSVSVSLITLYSHTVALSLKEHLADCLDKDYDTLLQTLQTLNGLPHINTSH 60
Db 1 MNLHVWKLSVSVSLITLYSHTVALSLKEHLADCLDKDYDTLLQTLQTLNGLPHINTSH 60
Oy 61 HWIVGAGMAGLTAALKLQDAGHTVTILEANDRVGGRVETVYRNEKEGWAEMGARIPSS 120

Db 61 HVVIVGAGMAGLTAAKLLQDAGHTVTILEANDRVGRVETRYNEKEGWAEMGAMRIPSS 120
Qy 121 HRIVQWFKVLGVENNEFVMTDDNTFYLVNGVRERTYVQENPDVLYKNVSESEKIGISAD 180
Db 121 HRIVQWFKVLGVENNEFVMTDDNTFYLVNGVRERTYVQENPDVLYKNVSESEKIGISAD 180
Qy 181 DLLDRALQKVKEVEANGKAALEKYDRYSVKEYLKEGGGLSPGAVRMIGDILLNEQSLMY 240
Db 181 DLLDRALQKVKEVEANGKAALEKYDRYSVKEYLKEGGGLSPGAVRMIGDILLNEQSLMY 240
Qy 241 TALSEMIYDQADVNDVSVTYHEVTGSDLLPEAFSLVLDVPILLNSKVKHIRQSDKGIVTS 300
Db 241 TALSEMIYDQADVNDVSVTYHEVTGSDLLPEAFSLVLDVPILLNSKVKHIRQSDKGIVTS 300
Qy 301 YOTGNESLMDSADIVLVTITAKAALFIDFDPPLSISKMEALRSVHYDSSTKILLTPRD 360
Db 301 YOTGNESLMDSADIVLVTITAKAALFIDFDPPLSISKMEALRSVHYDSSTKILLTPRD 360
Qy 361 KFWEDDGIRGKSIIDGSPRYIYYPSPHPTNETIGVLLASYTWSDESLLFLGASDEBLK 420
Db 361 KFWEDDGIRGKSIIDGSPRYIYYPSPHPTNETIGVLLASYTWSDESLLFLGASDEBLK 420
Qy 421 ELALRDLAKIHGEQVWDKCTGVIWKWSADPYSLGAFALFTPYQHLEYAQBELFSSEGRVH 480
Db 421 ELALRDLAKIHGEQVWDKCTGVIWKWSADPYSLGAFALFTPYQHLEYAQBELFSSEGRVH 480
Qy 481 FAGEHTAPPHAWIETSMKSAIRAATNINKVANEESTIHTKDEL 524
Db 481 FAGEHTAPPHAWIETSMKSAIRAATNINKVANEESTIHTKDEL 524

RESULT 2

US-10-644-142-1

; Sequence 1, Application US/10644142
; Publication No. US20040054147A1

; GENERAL INFORMATION:

; APPLICANT: Iwamoto, Mitsunori; Jung, Sang-Kee

; TITLE OF INVENTION: NOVEL PROTEIN, ITS GENE, REAGENTS FOR INDUCING

; FILE REFERENCE: 4703/0F214

; CURRENT APPLICATION NUMBER: US/10/644,142

; PRIOR FILING DATE: 2003-08-20

; PRIOR APPLICATION NUMBER: US/09/230,388

; PRIOR FILING DATE: 1999-01-22

; PRIOR APPLICATION NUMBER: PCT/JP98/02261

; NUMBER OF SEQ ID NOS: 2

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 1

; TYPE: PRT

; ORGANISM: Scomber japonicus

US-10-644-142-1

Query Match 100.0%; Score 2703; DB 15; Length 524;
Best Local Similarity 100.0%; Pred. No. 1.3e-216;
Matches 524; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MNLHVVKWKLVSVVSLITLYSHTVALSLKEHLADCLDKDYDTLLQTLNDGLPHINTSH 60
Db 1 MNLHVVKWKLVSVVSLITLYSHTVALSLKEHLADCLDKDYDTLLQTLNDGLPHINTSH 60
Qy 61 HVVIVGAGMAGLTAAKLLQDAGHTVTILEANDRVGRVETRYNEKEGWAEMGAMRIPSS 120
Db 61 HVVIVGAGMAGLTAAKLLQDAGHTVTILEANDRVGRVETRYNEKEGWAEMGAMRIPSS 120
Qy 121 HRIVQWFKVLGVENNEFVMTDDNTFYLVNGVRERTYVQENPDVLYKNVSESEKIGISAD 180
Db 121 HRIVQWFKVLGVENNEFVMTDDNTFYLVNGVRERTYVQENPDVLYKNVSESEKIGISAD 180
Qy 181 DLLDRALQKVKEVEANGKAALEKYDRYSVKEYLKEGGGLSPGAVRMIGDILLNEQSLMY 240
Db 181 DLLDRALQKVKEVEANGKAALEKYDRYSVKEYLKEGGGLSPGAVRMIGDILLNEQSLMY 240

Qy 241 TALSEMIYDQADVNDVSVTYHEVTGSDLLPEAFSLVLDVPILLNSKVKHIRQSDKGIVTS 300
Db 241 TALSEMIYDQADVNDVSVTYHEVTGSDLLPEAFSLVLDVPILLNSKVKHIRQSDKGIVTS 300
Qy 301 YOTGNESLMDSADIVLVTITAKAALFIDFDPPLSISKMEALRSVHYDSSTKILLTPRD 360
Db 301 YOTGNESLMDSADIVLVTITAKAALFIDFDPPLSISKMEALRSVHYDSSTKILLTPRD 360
Qy 361 KFWEDDGIRGKSIIDGSPRYIYYPSPHPTNETIGVLLASYTWSDESLLFLGASDEBLK 420
Db 361 KFWEDDGIRGKSIIDGSPRYIYYPSPHPTNETIGVLLASYTWSDESLLFLGASDEBLK 420
Qy 421 ELALRDLAKIHGEQVWDKCTGVIWKWSADPYSLGAFALFTPYQHLEYAQBELFSSEGRVH 480
Db 421 ELALRDLAKIHGEQVWDKCTGVIWKWSADPYSLGAFALFTPYQHLEYAQBELFSSEGRVH 480
Qy 481 FAGEHTAPPHAWIETSMKSAIRAATNINKVANEESTIHTKDEL 524
Db 481 FAGEHTAPPHAWIETSMKSAIRAATNINKVANEESTIHTKDEL 524

RESULT 3

US-10-645-094-1

; Sequence 1, Application US/10645094

; Publication No. US20050191737A1

; GENERAL INFORMATION:

; APPLICANT: Iwamoto, Mitsunori; Jung, Sang-Kee

; TITLE OF INVENTION: NOVEL PROTEIN, ITS GENE, REAGENTS FOR INDUCING

; FILE REFERENCE: 4703/0F214

; CURRENT APPLICATION NUMBER: US/10/645,094

; CURRENT FILING DATE: 2003-08-21

; PRIOR FILING DATE: 2001-07-24

; PRIOR APPLICATION NUMBER: US/09/230,388

; PRIOR FILING DATE: 1999-01-22

; PRIOR APPLICATION NUMBER: PCT/JP98/02261

; NUMBER OF SEQ ID NOS: 2

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 1

; TYPE: PRT

; ORGANISM: Scomber japonicus

US-10-645-094-1

Query Match 100.0%; Score 2703; DB 18; Length 524;
Best Local Similarity 100.0%; Pred. No. 1.3e-216;
Matches 524; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MNLHVVKWKLVSVVSLITLYSHTVALSLKEHLADCLDKDYDTLLQTLNDGLPHINTSH 60
Db 1 MNLHVVKWKLVSVVSLITLYSHTVALSLKEHLADCLDKDYDTLLQTLNDGLPHINTSH 60
Qy 61 HVVIVGAGMAGLTAAKLLQDAGHTVTILEANDRVGRVETRYNEKEGWAEMGAMRIPSS 120
Db 61 HVVIVGAGMAGLTAAKLLQDAGHTVTILEANDRVGRVETRYNEKEGWAEMGAMRIPSS 120
Qy 121 HRIVQWFKVLGVENNEFVMTDDNTFYLVNGVRERTYVQENPDVLYKNVSESEKIGISAD 180
Db 121 HRIVQWFKVLGVENNEFVMTDDNTFYLVNGVRERTYVQENPDVLYKNVSESEKIGISAD 180
Qy 181 DLLDRALQKVKEVEANGKAALEKYDRYSVKEYLKEGGGLSPGAVRMIGDILLNEQSLMY 240
Db 181 DLLDRALQKVKEVEANGKAALEKYDRYSVKEYLKEGGGLSPGAVRMIGDILLNEQSLMY 240
Qy 241 TALSEMIYDQADVNDVSVTYHEVTGSDLLPEAFSLVLDVPILLNSKVKHIRQSDKGIVTS 300
Db 241 TALSEMIYDQADVNDVSVTYHEVTGSDLLPEAFSLVLDVPILLNSKVKHIRQSDKGIVTS 300
Qy 301 YOTGNESLMDSADIVLVTITAKAALFIDFDPPLSISKMEALRSVHYDSSTKILLTPRD 360
Db 301 YOTGNESLMDSADIVLVTITAKAALFIDFDPPLSISKMEALRSVHYDSSTKILLTPRD 360

Db 301 YQTGNESSLMDLSADIVLVTTTAKAALFIDFDPPLSISKMEALRSVHYDSSTKILLTFRD 360
Qy 361 KFWEDDGIRGKSIITDGPRIYIYPGSHSFHTNETIGVLLASYTWSDESLLFLGASDEELK 420
Db 361 KFWEDDGIRGKSIITDGPRIYIYPGSHSFHTNETIGVLLASYTWSDESLLFLGASDEELK 420
Qy 421 ELALRDLAKIHGEQWWDKCTGVIVKWSADPYSLGAFALFTPYQHLEYAQELFSSEGRVH 480
Db 421 ELALRDLAKIHGEQWWDKCTGVIVKWSADPYSLGAFALFTPYQHLEYAQELFSSEGRVH 480
Qy 481 FAGEHTAFPHAMTETSMKSAIRAATNINKVANEESTIETHTKDEL 524
Db 481 FAGEHTAFPHAMTETSMKSAIRAATNINKVANEESTIETHTKDEL 524

RESULT 4
US-09-938-795A-1
; Sequence 1, Application US/09938795A
; Publication No. US20030045688A1
; GENERAL INFORMATION:
; APPLICANT: CHU, CHARLES CHIYUAN
; APPLICANT: CHAVAN, SANGEETA S.
; APPLICANT: MASON, JAMES M.
; TITLE OF INVENTION: HUMAN INTERLEUKIN-FOUR INDUCED PROTEIN
; FILE REFERENCE: LIJ-9000-US
; CURRENT APPLICATION NUMBER: US/09/938,795A
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: 60/227,818
; PRIOR FILING DATE: 2000-08-25
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 630
; TYPE: PRT
; ORGANISM: Mus sp.
US-09-938-795A-1

Query Match 38.3%; Score 1034; DB 10; Length 630;
Best Local Similarity 43.5%; Pred. No. 3.9e-77;
Matches 212; Conservative 100; Mismatches 163; Indels 12; Gaps 6;
Qy 26 ALSLKEHLADCLDEDKYDTLLQTLONGPLPHINTSHHVIYVAGMAGLTAAKLLQDAGHTV 85
Db 25 AASLNPISKECMHEDHYEQLLKVTLLNRTSKPKQVYVVGAGVAGLVAAKMLSDAGHKV 84
Qy 86 TLEANDRVGGRVETVYRNEKEGWYAEWGAMRTPSSSHRIVQWFKLVGMENFEVMTDDNT 145
Db 85 TLEADNRIGGRIFTRDEKGTWIGELGAMRWPSSHRILHUKCRTLGLNLTOTFYQDENT 144
Qy 146 FYLVNGVRERTYVVOENPDVLKYNVSESEKGISADDDLDRLAQKVKEEVEANGCKAALEK 205
Db 145 MTEVHNVLKRNYYVEKMPKGLYNLNNRERGHSPEDIYQMALNKAFKOLKALGCKKAMNK 204
Qy 206 YDRYSVKEVLEEGGLSGPAGVMIGDGLNEQSLMTALSEMIYDQADVNDVSYHYEVTGG 265
Db 205 FNKHTLLEYLLBEGNLSRPVQLLGDVMSSEEGFFYLSFAEALRAHACLSRLRYSRIVGG 264
Qy 266 SDLLPEAFSLVDVPTLLNSKVKHIRQSDKGVIVSYQVTGNESSLMDLSADIVLVTTTAKA 325
Db 265 WDLPLRALLSSUSGALLNAPVVSITQGRNDRVHIATSLHSE-KTLTADVVLLTASGPA 323
Qy 326 ALFIDFDPPLSISKMEALRSVHYDSSTKILLTFRDKFWEDDGIRGKSIITDGPRIYIYP 385
Db 324 LQRIITFSPPLTRKQERQALRALHYVAASKVFLSFRFPFWHEEHIEGHNSNDRPSRLIFYP 383
Qy 386 SHSFHTNETIGVLLASYTWSDESLLFLGASDEELKELALRDLAKIHGE---QVWDKCTGV 442
Db 384 ARGEKS-----LLLASYTWSDAAPFAGLSTQTLRLVLQDVAALHGPVWFLWDG-RGV 437
Qy 443 IVKWSADPYSLGAFALFTPYQHLEYAQELFSSE-GRVHFACEHTAFPHAMTETSMKSAI 501
Db 438 -VKRWAEDPHSGGFWQPPVGLYGREADYDWSAPFGRIYFAGEHTALPHGWVETAVKSGL 496

Qy 502 RAATNIN 508
Db 497 RAAVRIN 503

RESULT 5
US-09-938-795A-2
; Sequence 2, Application US/09938795A
; Publication No. US20030045688A1
; GENERAL INFORMATION:
; APPLICANT: CHU, CHARLES CHIYUAN
; APPLICANT: CHAVAN, SANGEETA S.
; APPLICANT: MASON, JAMES M.
; TITLE OF INVENTION: HUMAN INTERLEUKIN-FOUR INDUCED PROTEIN
; FILE REFERENCE: LIJ-9000-US
; CURRENT APPLICATION NUMBER: US/09/938,795A
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: 60/227,818
; PRIOR FILING DATE: 2000-08-25
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 567
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-938-795A-2

Query Match 37.0%; Score 999; DB 10; Length 567;
Best Local Similarity 41.8%; Pred. No. 2.8e-74;
Matches 217; Conservative 99; Mismatches 171; Indels 32; Gaps 9;
Qy 3 LHVVKWKLSSVSVLITLYYSHT-VALSLKEHLADCLDEDKYDTLLQTLONGPLPHINTSHH 61
Db 6 LHL-----LVLPILLSLVASQDQWKAERSQSDPEKCKWQPDYEQLLKVVWTGLNRTLKPQR 61
Qy 62 VIVVAGMAGLTAAKLLQDAGHTVITLEANDRVGGRVETVYRNEKEGWYAEWGAMRIPSSH 121
Db 62 VIVVAGVAGLVAAKVLSDAGHKVITLEADNRIGRIFTYRQNTGTWIGELGAMRMPSSH 121
Qy 122 RIVQWFKLVGMENFEVMTDDNTFVNGVRYRRTYVVOENPDVLKYNVSESEKGISADD 181
Db 122 RILHKLCOGLGULNLTFTQYDKNTWTEVHEVKLRNYYVEKVKUGYALRPOEKHSPED 181
Qy 182 LLDRLAQKVKEEVEANGCKAALEKDYRSVKEYLKEEGGLSGPAGVMIGDGLNEQSLMT 241
Db 182 IYQWALNQAALKDLKALGCRKAMKKEFHTLLEYLLGEGNLSRPAVQLLGDVMSDEGFFYL 241
Qy 242 ALSEMIYDQADVNDVSYHYEVTGSDLLPEAFSLVDVPTLLNSKVKHIRQSDKGVIVSY 301
Db 242 SFAEALRAHSCLSRLRYSRIVGGWDLPLRALLSSLSGLVLLNAPVWAMTQPHDVHVOI 301
Qy 302 QTGNES-SLMDLSADIVLVTTTAKAALFIDFDPPLSISKMEALRSVHYDSSTKILLTFRD 360
Db 302 ETSPPARNLKVLDKADVLLTASGPAVKRITPSPPLRHMQLRRLHLYVPATKVFLSFR 361
Qy 361 KFWEDDGIRGKSIITDGPRIYIYPGSHSFHTNETIGVLLASYTWSDESLLFLGASDEELK 420
Db 362 FFWHEEHIEGHNSNDRPSRLIFYP-----PPREGALLASYTWSDAAPFAGLSREAL 416
Qy 421 ELALRDLAKIHGE---EQWWDKCTGVIVKWSADPYSLGAFALFTPYQHLEYAQELFSSE- 476
Db 417 RLALDDVAALHGPVVRQLWDG-TGV-VKRWAEDQHSQSGFVVVQPP-----ALMQTEK 466
Qy 477 -----GRVHFACEHTAFPHAMTETSMKSAIRAATNIN 508
Db 467 DDWTVPYGRIYFAGEHTAIPHGWVETAVKLSALRAAIKIN 505

RESULT 6
US-09-946-374-84
; Sequence 84, Application US/09946374
; Publication No. US20030073129A1
; GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2830P1C1
CURRENT APPLICATION NUMBER: US/09/946,374
CURRENT FILING DATE: 2001-09-04
PRIOR APPLICATION NUMBER: 60/098716
PRIOR FILING DATE: 1998-09-01
PRIOR APPLICATION NUMBER: 60/098723
PRIOR FILING DATE: 1998-09-01
PRIOR APPLICATION NUMBER: 60/098749
PRIOR FILING DATE: 1998-09-01
PRIOR APPLICATION NUMBER: 60/098750
PRIOR FILING DATE: 1998-09-01
PRIOR APPLICATION NUMBER: 60/098803
PRIOR FILING DATE: 1998-09-02
PRIOR APPLICATION NUMBER: 60/098821
PRIOR FILING DATE: 1998-09-02
PRIOR APPLICATION NUMBER: 60/098843
PRIOR FILING DATE: 1998-09-02
PRIOR APPLICATION NUMBER: 60/099536
PRIOR FILING DATE: 1998-09-09
PRIOR APPLICATION NUMBER: 60/099596
PRIOR FILING DATE: 1998-09-09
PRIOR APPLICATION NUMBER: 60/099598
PRIOR FILING DATE: 1998-09-09
PRIOR APPLICATION NUMBER: 60/099602
PRIOR FILING DATE: 1998-09-09
PRIOR APPLICATION NUMBER: 60/099642
PRIOR FILING DATE: 1998-09-09
PRIOR APPLICATION NUMBER: 60/099741
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: 60/099754
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: 60/099763
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: 60/099792
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: 60/099808
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: 60/099812
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: 60/099815
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: 60/099816
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: 60/100385
PRIOR FILING DATE: 1998-09-15
PRIOR APPLICATION NUMBER: 60/100388
PRIOR FILING DATE: 1998-09-15
PRIOR APPLICATION NUMBER: 60/100390
PRIOR FILING DATE: 1998-09-15
PRIOR APPLICATION NUMBER: 60/100584
PRIOR FILING DATE: 1998-09-30
PRIOR APPLICATION NUMBER: 60/100627
PRIOR FILING DATE: 1998-09-16
PRIOR APPLICATION NUMBER: 60/100661
PRIOR FILING DATE: 1998-09-16
PRIOR APPLICATION NUMBER: 60/100662
PRIOR FILING DATE: 1998-09-16
PRIOR APPLICATION NUMBER: 60/100664
PRIOR FILING DATE: 1998-09-16
PRIOR APPLICATION NUMBER: 60/100683
PRIOR FILING DATE: 1998-09-17
PRIOR APPLICATION NUMBER: 60/100684
PRIOR FILING DATE: 1998-09-17
PRIOR APPLICATION NUMBER: 60/100710
PRIOR FILING DATE: 1998-09-17
PRIOR APPLICATION NUMBER: 60/100711
PRIOR FILING DATE: 1998-09-17
PRIOR APPLICATION NUMBER: 60/100848
PRIOR FILING DATE: 1998-09-18
PRIOR APPLICATION NUMBER: 60/100849
PRIOR FILING DATE: 1998-09-18
PRIOR APPLICATION NUMBER: 60/100919
PRIOR FILING DATE: 1998-09-17
PRIOR APPLICATION NUMBER: 60/100930
PRIOR FILING DATE: 1998-09-17
PRIOR APPLICATION NUMBER: 60/101014
PRIOR FILING DATE: 1998-09-18
PRIOR APPLICATION NUMBER: 60/101068
PRIOR FILING DATE: 1998-09-18
PRIOR APPLICATION NUMBER: 60/101071
PRIOR FILING DATE: 1998-09-18
PRIOR APPLICATION NUMBER: 60/101279
PRIOR FILING DATE: 1998-09-22
PRIOR APPLICATION NUMBER: 60/101471
PRIOR FILING DATE: 1998-09-23
PRIOR APPLICATION NUMBER: 60/101472
PRIOR FILING DATE: 1998-09-23
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PRIOR APPLICATION NUMBER: 60/101477
PRIOR FILING DATE: 1998-09-23
PRIOR APPLICATION NUMBER: 60/101479
PRIOR FILING DATE: 1998-09-23
PRIOR APPLICATION NUMBER: 60/101738
PRIOR FILING DATE: 1998-09-24
PRIOR APPLICATION NUMBER: 60/101741
PRIOR FILING DATE: 1998-09-24
PRIOR APPLICATION NUMBER: 60/101743
PRIOR FILING DATE: 1998-09-24
PRIOR APPLICATION NUMBER: 60/101915
PRIOR FILING DATE: 1998-09-24
PRIOR APPLICATION NUMBER: 60/101916
PRIOR FILING DATE: 1998-09-24
PRIOR APPLICATION NUMBER: 60/102207
PRIOR FILING DATE: 1998-09-29
PRIOR APPLICATION NUMBER: 60/102240
PRIOR FILING DATE: 1998-09-29
PRIOR APPLICATION NUMBER: 60/102307
PRIOR FILING DATE: 1998-09-29
PRIOR APPLICATION NUMBER: 60/102330
PRIOR FILING DATE: 1998-09-29
PRIOR APPLICATION NUMBER: 60/102331
PRIOR FILING DATE: 1998-09-29
PRIOR APPLICATION NUMBER: 60/102484
PRIOR FILING DATE: 1998-09-30
PRIOR APPLICATION NUMBER: 60/102487
PRIOR FILING DATE: 1998-09-30
PRIOR APPLICATION NUMBER: 60/102570
PRIOR FILING DATE: 1998-09-30

1	PRIOR APPLICATION NUMBER:	60/102571
2	PRIOR FILING DATE:	1998-09-30
3	PRIOR APPLICATION NUMBER:	60/102684
4	PRIOR FILING DATE:	1998-10-01
5	PRIOR APPLICATION NUMBER:	60/102687
6	PRIOR FILING DATE:	1998-10-01
7	PRIOR APPLICATION NUMBER:	60/102965
8	PRIOR FILING DATE:	1998-10-02
9	PRIOR APPLICATION NUMBER:	60/103258
10	PRIOR FILING DATE:	1998-10-06
11	PRIOR APPLICATION NUMBER:	60/103314
12	PRIOR FILING DATE:	1998-10-07
13	PRIOR APPLICATION NUMBER:	60/103315
14	PRIOR FILING DATE:	1998-10-07
15	PRIOR APPLICATION NUMBER:	60/103328
16	PRIOR FILING DATE:	1998-10-07
17	PRIOR APPLICATION NUMBER:	60/103395
18	PRIOR FILING DATE:	1998-10-07
19	PRIOR APPLICATION NUMBER:	60/103396
20	PRIOR FILING DATE:	1998-10-07
21	PRIOR APPLICATION NUMBER:	60/103401
22	PRIOR FILING DATE:	1998-10-07
23	PRIOR APPLICATION NUMBER:	60/103449
24	PRIOR FILING DATE:	1998-10-06
25	PRIOR APPLICATION NUMBER:	60/103633
26	PRIOR FILING DATE:	1998-10-08
27	PRIOR APPLICATION NUMBER:	60/103678
28	PRIOR FILING DATE:	1998-10-08
29	PRIOR APPLICATION NUMBER:	60/103679
30	PRIOR FILING DATE:	1998-10-08
31	PRIOR APPLICATION NUMBER:	60/103711
32	PRIOR FILING DATE:	1998-10-08
33	PRIOR APPLICATION NUMBER:	60/104257
34	PRIOR FILING DATE:	1998-10-14
35	PRIOR APPLICATION NUMBER:	60/104987
36	PRIOR FILING DATE:	1998-10-20
37	PRIOR APPLICATION NUMBER:	60/105000
38	PRIOR FILING DATE:	1998-10-20
39	PRIOR APPLICATION NUMBER:	60/105002
40	PRIOR FILING DATE:	1998-10-20
41	PRIOR APPLICATION NUMBER:	60/105104
42	PRIOR FILING DATE:	1998-10-21
43	PRIOR APPLICATION NUMBER:	60/105169
44	PRIOR FILING DATE:	1998-10-22
45	PRIOR APPLICATION NUMBER:	60/105266
46	PRIOR FILING DATE:	1998-10-22
47	PRIOR APPLICATION NUMBER:	60/105693
48	PRIOR FILING DATE:	1998-10-26
49	PRIOR APPLICATION NUMBER:	60/105694
50	PRIOR FILING DATE:	1998-10-26
51	PRIOR APPLICATION NUMBER:	60/105907

Query Match 37.0%; Score 999; DB 10; Length 567;

Best Local Similarity 41.8%; Pred. No. 2.8e-74;

Matches	217;	Conservative	99;	Mismatches	171;	Indels	32;	Gaps	9;
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Qy	3	LHVWVKLSVSVLTLVYSHT- VALSKEHLACLEDKDYDTLLQTLDNGLPHINTSHH	61
Db	6	LHL-----LVLPILLSVASODWAERSQDPFEXCMQDPDYEQLLKVTVVTWNLRTLPQR	61
Qy	62	VVIVGAGMAGLTAALKQDAGHTVTLLEANDRVGGRVETVYRNEKEGWYAEMGAMRIPSSH	121
Db	62	VIVUGAGVAGLVAAKVLSDAGHKVTLLEADNRIIGRIFTYRDQNTGMI GELGAWRPPSH	121
Qy	122	RIVOFVFKLGVEMNEFVMTDDNTFYLVNGVRETRYVVOENPVLKYNVSESEKGSADD	181
Db	122	RIHLKLCQGLNLTKFTQYDKNTWTEVHEVKLRNVYVVEKPEKLYALRPQEKHSPED	181
Qy	182	LLDRALKQVKEVEANGCAALEKVDKYSVKEYLKESGGLSPGAVRMI GDLLNEQSLMT	241
Db	182	IYQMALNQALKDLKALGCRKAMKPFERHTLLEYLLGEGNLSRPAVOLLLGVWSEDFYFL	241
Qy	242	ALSEMIYDQADVNDVSVTYVHEVTGGSDLLPEAFVSLVDVPILLNSKVYKHTRQSDKGVISY	301

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/ PRIOR APPLICATION NUMBER: 60/108849
/ PRIOR FILING DATE: 1998-11-18
/ PRIOR APPLICATION NUMBER: 60/112420
/ PRIOR FILING DATE: 1998-12-15
/ PRIOR APPLICATION NUMBER: 60/113296
/ PRIOR FILING DATE: 1998-12-22
/ PRIOR APPLICATION NUMBER: 60/115554
/ PRIOR FILING DATE: 1999-01-12
/ PRIOR APPLICATION NUMBER: 60/115558
/ PRIOR FILING DATE: 1999-01-12
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/ PRIOR FILING DATE: 1999-01-20
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/ PRIOR FILING DATE: 1999-03-10
/ PRIOR APPLICATION NUMBER: 60/131294
/ PRIOR FILING DATE: 1999-04-07
/ PRIOR APPLICATION NUMBER: 60/140650
/ PRIOR FILING DATE: 1999-06-22
/ PRIOR APPLICATION NUMBER: 60/141037
/ PRIOR FILING DATE: 1999-06-23
/ PRIOR APPLICATION NUMBER: 60/144758
/ PRIOR FILING DATE: 1999-07-20
/ PRIOR APPLICATION NUMBER: 60/162506
/ PRIOR FILING DATE: 1999-10-29
/ PRIOR APPLICATION NUMBER: 60/170262
/ PRIOR FILING DATE: 1999-12-09
/ PRIOR APPLICATION NUMBER: 60/187202
/ PRIOR FILING DATE: 2000-03-03
/ PRIOR APPLICATION NUMBER: 60/209832
/ PRIOR FILING DATE: 2000-06-05
/ PRIOR APPLICATION NUMBER: 60/232887
/ PRIOR FILING DATE: 2000-09-15
/ PRIOR APPLICATION NUMBER: 09/180997
/ PRIOR FILING DATE: 1998-11-19
/ PRIOR APPLICATION NUMBER: 09/218517
/ PRIOR FILING DATE: 1998-12-22
/ PRIOR APPLICATION NUMBER: 09/284291
/ PRIOR FILING DATE: 1999-04-12
/ PRIOR APPLICATION NUMBER: 09/380137
/ PRIOR FILING DATE: 1999-08-25
/ PRIOR APPLICATION NUMBER: 09/380138
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/ PRIOR FILING DATE: 2001-06-14
/ PRIOR APPLICATION NUMBER: 09/918585
/ PRIOR FILING DATE: 2001-07-30
/ PRIOR APPLICATION NUMBER: 09/924419
/ PRIOR FILING DATE: 2001-08-06
/ PRIOR APPLICATION NUMBER: 09/927796
/ PRIOR FILING DATE: 2001-08-06
/ PRIOR APPLICATION NUMBER: 09/929404
/ PRIOR FILING DATE: 2001-08-13
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/ PRIOR FILING DATE: 2001-08-28
/ PRIOR APPLICATION NUMBER: 09/946374
/ PRIOR FILING DATE: 2001-09-04
/ PRIOR APPLICATION NUMBER: PCT/US98/18824
/ PRIOR FILING DATE: 1998-09-10
/ PRIOR APPLICATION NUMBER: PCT/US99/00106
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/ PRIOR FILING DATE: 1999-01-05
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/ PRIOR FILING DATE: 1999-03-08
/ PRIOR APPLICATION NUMBER: PCT/US99/08615
/ PRIOR FILING DATE: 1999-04-20
/ PRIOR APPLICATION NUMBER: PCT/US99/12252
/ PRIOR FILING DATE: 1999-06-02
/ PRIOR APPLICATION NUMBER: PCT/US99/20111
/ PRIOR FILING DATE: 1999-09-01
/ PRIOR APPLICATION NUMBER: PCT/US99/20594
/ PRIOR FILING DATE: 1999-09-08
/ PRIOR APPLICATION NUMBER: PCT/US99/28313
/ PRIOR FILING DATE: 1999-11-30
/ PRIOR APPLICATION NUMBER: PCT/US99/28551
/ PRIOR FILING DATE: 1999-12-02
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/ PRIOR FILING DATE: 1999-12-16
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/ PRIOR APPLICATION NUMBER: PCT/US00/00376
/ PRIOR FILING DATE: 2000-01-06
/ PRIOR APPLICATION NUMBER: PCT/US00/03565
/ PRIOR FILING DATE: 2000-02-11
/ PRIOR APPLICATION NUMBER: PCT/US00/04341
/ PRIOR FILING DATE: 2000-02-18
/ PRIOR APPLICATION NUMBER: PCT/US00/04342
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/ PRIOR APPLICATION NUMBER: PCT/US00/06884
/ PRIOR FILING DATE: 2000-03-15
/ PRIOR APPLICATION NUMBER: PCT/US00/08439
/ PRIOR FILING DATE: 2000-03-30
/ PRIOR APPLICATION NUMBER: PCT/US00/13705
/ PRIOR FILING DATE: 2000-05-17
/ PRIOR APPLICATION NUMBER: PCT/US00/14042
/ PRIOR FILING DATE: 2000-05-22
/ PRIOR APPLICATION NUMBER: PCT/US00/14941
/ PRIOR FILING DATE: 2000-05-30
/ PRIOR APPLICATION NUMBER: PCT/US00/15264
/ PRIOR FILING DATE: 2000-06-02
/ PRIOR APPLICATION NUMBER: PCT/US00/22031
/ PRIOR FILING DATE: 2000-08-11
/ PRIOR APPLICATION NUMBER: PCT/US00/23522
/ PRIOR FILING DATE: 2000-08-23
/ PRIOR APPLICATION NUMBER: PCT/US00/30873
/ PRIOR FILING DATE: 2000-11-10
/ PRIOR APPLICATION NUMBER: PCT/US00/32678
/ PRIOR FILING DATE: 2000-12-01
/ PRIOR APPLICATION NUMBER: PCT/US01/06520
/ PRIOR FILING DATE: 2001-02-28
/ PRIOR APPLICATION NUMBER: PCT/US01/06666
/ PRIOR FILING DATE: 2001-03-01
/ PRIOR APPLICATION NUMBER: PCT/US01/17092
/ PRIOR FILING DATE: 2001-05-25
/ PRIOR APPLICATION NUMBER: PCT/US01/17800
/ PRIOR FILING DATE: 2001-06-01
/ PRIOR APPLICATION NUMBER: PCT/US01/19692
/ PRIOR FILING DATE: 2001-06-20
/ PRIOR APPLICATION NUMBER: PCT/US01/21066
/ PRIOR FILING DATE: 2001-06-29
/ PRIOR APPLICATION NUMBER: PCT/US01/21735
/ PRIOR FILING DATE: 2001-07-09
/ PRIOR APPLICATION NUMBER: PCT/US01/27099
/ PRIOR FILING DATE: 2001-08-29
/ NUMBER OF SEQ ID NOS: 91
/ SEQ ID NO 24
/ LENGTH: 567
/ TYPE: PRT
/ ORGANISM: Homo Sapien
US-10-001-054-24
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Query Match 37.0%; Score 999; DB 13; Length 567;
Best Local Similarity 41.8%; Pred. No. 2.8e-74;
Matches 217; Conservative 99; Mismatches 171; Indels 32; Gaps 9;

Qy 3 LHVVKVSVVSVLITLYSHT-VALSLKEHLADCLDQDYDTLQTLQDGLPHINTSHH 61
Db 6 LHL-----LVLVPIILLSVASQDWKASQDPFEKQMDPDYEQLLKVVVTWGLNRTLKPOR 61

Qy 62 VVIVGAGMAGLTAAKLLQDAGHTVTILEANDRVGGRVETRYNEKEGWAEKMGAMRIPSSH 121
Db 62 VVIVGAGVAGLVAAKVLSDAGHKVTILEADNRIGRIFFYRDQNTGWTGELGAMRMPSSH 121

Qy 122 RIVQFVKVLGVMEFVMTDNTFYLNGVRERTYVVOENPDVLKYNVSEKGISADD 181
Db 122 RILHLKLCQGLGLNLTFTQYDKNTWTEVHEVKLRNVVVEKPEKLGALRPOEKHSPED 181

Qy 182 LLDRLALQKVEEVEANGCKAALEKYDRYSVKEYLKEEGSLSPGAVRMTGDLNQSMT 241
Db 182 IYQMALNQALKDLKALGCRKAMKFERHTLLEYLLGEGNLSRPAVQLLDGVMSDEGFFYL 241

Qy 242 ALSEMIYDQADVNDVSTYHEVTGGSDLLPEAFSLVDVPIILLNSKVKHIRQSDKGVISY 301
Db 242 SFAEALRAHSCUSDRLOYSRIVGGWDLPRALLSSGLVLLNAPVAVMTQGHVDHVOI 301

Qy 302 QTGNES-SLMDLSADIVLVTAKAALFIDFPPPLSISKWEALRSVHYDSSTKILLTFRD 360
Db 302 ETSPPARNLKVLDVLLTASGPAVKRITFPPLPRHMQEALRLHYVPATKVFLSFR 361

Qy 361 KFWEDDGIKGSITDGPRIYYPSSHFTNETGVLLASVTWSDSLLFLGASDEELK 420
Db 362 PFWREEHIEGHSNTRDPSRMIFYP-----PPREGALLASVTWSDAAAFAGLSREAL 416

Qy 421 ELALRDLAKIHG---EOWDKCTGVIVKWSADPYSLGAFALFTPYQHLEYAQELFSSE- 476
Db 417 RLALDDVAAALRGVVRVQLWDG-TGV-VKRWAEQHSQGGFVVQPP-----ALWQTEK 466

Qy 477 -----GRVHPAGEHTAPPHAWIETSMKSASRAATNIN 508
Db 467 DDMVTVPYGRYIYFAGEHTAVPHGMVETAVKSALRAIKIN 505

RESULT 8
US-10-053-107-2
; Sequence 2, Application US/10053107
; Publication No. US20020192752A1
; GENERAL INFORMATION:
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Compositions and Methods for the Treatment of Immune
; TITLE OF INVENTION: Related Diseases
; FILE REFERENCE: P3033R1C1
; CURRENT APPLICATION NUMBER: US/10/053,107
; CURRENT FILING DATE: 2002-01-17
; PRIOR APPLICATION NUMBER: 60/099601
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/107783
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: 60/108802
; PRIOR FILING DATE: 1998-11-17
; PRIOR APPLICATION NUMBER: 60/113296
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: 60/131291
; PRIOR FILING DATE: 1999-04-27
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; PRIOR APPLICATION NUMBER: 60/232887
; PRIOR FILING DATE: 2000-09-15
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; PRIOR FILING DATE: 1999-01-05
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; PRIOR FILING DATE: 1999-09-01
; PRIOR APPLICATION NUMBER: PCT/US00/04342
; PRIOR FILING DATE: 2000-02-18
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; PRIOR APPLICATION NUMBER: PCT/US00/13705
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; PRIOR FILING DATE: 2000-06-02
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; PRIOR FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: PCT/US00/23328
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: PCT/US01/17800
; PRIOR FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: PCT/US01/19692
; PRIOR FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: PCT/US01/21066
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: PCT/US01/21735
; PRIOR FILING DATE: 2001-07-09
; NUMBER OF SEQ ID NOS: 14
; SEQ ID NO 2
; LENGTH: 567
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-053-107-2

Query Match 37.0%; Score 999; DB 13; Length 567;
Best Local Similarity 41.8%; Pred. No. 2.8e-74;
Matches 217; Conservative 99; Mismatches 171; Indels 32; Gaps 9;

Qy 3 LHVVKVSVVSVLITLYSHT-VALSLKEHLADCLDQDYDTLQTLQDGLPHINTSHH 61
Db 6 LHL-----LVLVPIILLSVASQDWKASQDPFEKQMDPDYEQLLKVVVTWGLNRTLKPOR 61

Qy 62 VVIVGAGMAGLTAAKLLQDAGHTVTILEANDRVGGRVETRYNEKEGWAEKMGAMRIPSSH 121
Db 62 VVIVGAGVAGLVAAKVLSDAGHKVTILEADNRIGRIFFYRDQNTGWTGELGAMRMPSSH 121

Qy 122 RIVQFVKVLGVMEFVMTDNTFYLNGVRERTYVVOENPDVLKYNVSEKGISADD 181
Db 122 RILHLKLCQGLGLNLTFTQYDKNTWTEVHEVKLRNVVVEKPEKLGALRPOEKHSPED 181

Qy 182 LLDRLALQKVEEVEANGCKAALEKYDRYSVKEYLKEEGSLSPGAVRMTGDLNQSMT 241
Db 182 IYQMALNQALKDLKALGCRKAMKFERHTLLEYLLGEGNLSRPAVQLLDGVMSDEGFFYL 241

Qy 242 ALSEMIYDQADVNDVSTYHEVTGGSDLLPEAFSLVDVPIILLNSKVKHIRQSDKGVISY 301
Db 242 SFAEALRAHSCUSDRLOYSRIVGGWDLPRALLSSGLVLLNAPVAVMTQGHVDHVOI 301

Qy 302 QTGNES-SLMDLSADIVLVTAKAALFIDFPPPLSISKWEALRSVHYDSSTKILLTFRD 360
Db 302 ETSPPARNLKVLDVLLTASGPAVKRITFPPLPRHMQEALRLHYVPATKVFLSFR 361

Qy 361 KFWEDDGIKGSITDGPRIYYPSSHFTNETGVLLASVTWSDSLLFLGASDEELK 420
Db 362 PFWREEHIEGHSNTRDPSRMIFYP-----PPREGALLASVTWSDAAAFAGLSREAL 416

Qy 421 ELALRDLAKIHG---EOWDKCTGVIVKWSADPYSLGAFALFTPYQHLEYAQELFSSE- 476
Db 417 RLALDDVAAALRGVVRVQLWDG-TGV-VKRWAEQHSQGGFVVQPP-----ALWQTEK 466

Qy 477 -----GRVHPAGEHTAPPHAWIETSMKSASRAATNIN 508
Db 467 DDMVTVPYGRYIYFAGEHTAVPHGMVETAVKSALRAIKIN 505
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Oy 3 LHVWKLSVSVLITLYSHT-VALSLKEHLADCLDXYDTLLQTLNDGLPHINTSHH 61
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
6 LHL-----LVLPILLSVASQDWKAERSQDPPEKCMQDPDYEQLLKVVWTGLNRTLKPQR 61
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62 VVIVGAGMAGLTAALKLODAGHTVTILEANDRVGGRVETRYNEKEGYAEMGAMRIPSSH 121
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
62 VVIVGAGVAGLVAAKVLSDAGHKVTILEADNRIGGRIFTYRDQNTGIGELGAMRMPSSH 121
Oy : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
122 RIVQFVKVLGVEMNEFVMTDNTFYLVNGVRERYVVOENPDVLKYNVSESEKISADD 181
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
122 RILHKLCOGLGLNLTKFTQYDKNTWTEVHEVKLRNVYVEKPEKLGALRPOEKHSPED 181
Oy : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
182 LLDRLAQKVEBEANGCKAALKYDRYSVKEYLKEEGSLSPGAVRMIGDLINEOSLMYT 241
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
182 IYQMALNQALDKLKGCKKAMKFERHTLLEYLLGEGNLSRPAVQLLGDVMSDGFYL 241
Oy : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
242 ALSEMIYQADVNDVSYTHEVTGGSLLPEAFSLVDVPIILNSKVKHRSQDKGVIVSY 301
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
242 SFAALRAHSCSLDRLOYSRIVGGWDLPLRALLSLGLVLLNAPVAVMTQCPHDVHVOI 301
Oy : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
302 QTGNES-SLMDLSADIVLVTAKAALFIDPDPPLSISKMEALRSVHYDSSTKILLTFRD 360
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
302 ETSPPARNLKVLAADVLLTASGPAVKRITFSPPLPRHMQEALRLHYVPATKVFLSFRR 361
Oy : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
361 KFWEDDGIRGKSIITDGPSTYIYPSHSPHTNETIGVLLASYTWSDESLLFLGASDEELK 420
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362 PWRREHIEGHSNTDRPSRMIFYP-----PPREGALLASYTWSDAAGLRSREAL 416
Oy : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
421 ELALRDLAKIHG---EQWDKCTGVIVKWSADPYSLGAFALFTPYQHLEYAQLFSSE- 476
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
417 RLALDDVAALHGPVVRQLWDG-TGV-VKRWAEQHSQGFVVQPP-----ALWQTEK 466
Oy : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
477 -----GRVHFACEHTAFPHAWIETSMKSAIRAATNIN 508
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467 DDWTPYGRIFYAGEHTAYPHGWVETAVKSAALRAAIKIN 505
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RESULT 11

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US-10-121-049-476
; Sequence 476, Application US/10121049
; Publication No. US2003002239A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C17
; CURRENT APPLICATION NUMBER: US/10/121,049
; CURRENT FILING DATE: 2002-04-12
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 476
; LENGTH: 567
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-121-049-476
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Query Match 37.0%; Score 999; DB 14; Length 567;

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Best Local Similarity 41.8%; Pred. No. 2.8e-74;
Matches 217; Conservative 99; Mismatches 171; Indels 32; Gaps 9;
Oy 3 LHVWKLSVSVLITLYSHT-VALSLKEHLADCLDXYDTLLQTLNDGLPHINTSHH 61
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6 LHL-----LVLPILLSVASQDWKAERSQDPPEKCMQDPDYEQLLKVVWTGLNRTLKPQR 61
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62 VVIVGAGMAGLTAALKLODAGHTVTILEANDRVGGRVETRYNEKEGYAEMGAMRIPSSH 121
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
62 VVIVGAGVAGLVAAKVLSDAGHKVTILEADNRIGGRIFTYRDQNTGIGELGAMRMPSSH 121
Oy : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
122 RIVQFVKVLGVEMNEFVMTDNTFYLVNGVRERYVVOENPDVLKYNVSESEKISADD 181
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
122 RILHKLCOGLGLNLTKFTQYDKNTWTEVHEVKLRNVYVEKPEKLGALRPOEKHSPED 181
Oy : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
182 LLDRLAQKVEBEANGCKAALKYDRYSVKEYLKEEGSLSPGAVRMIGDLINEOSLMYT 241
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
182 IYQMALNQALDKLKGCKKAMKFERHTLLEYLLGEGNLSRPAVQLLGDVMSDGFYL 241
Oy : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
242 ALSEMIYQADVNDVSYTHEVTGGSLLPEAFSLVDVPIILNSKVKHRSQDKGVIVSY 301
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
242 SFAALRAHSCSLDRLOYSRIVGGWDLPLRALLSLGLVLLNAPVAVMTQCPHDVHVOI 301
Oy : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
302 QTGNES-SLMDLSADIVLVTAKAALFIDPDPPLSISKMEALRSVHYDSSTKILLTFRD 360
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
302 ETSPPARNLKVLAADVLLTASGPAVKRITFSPPLPRHMQEALRLHYVPATKVFLSFRR 361
Oy : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
361 KFWEDDGIRGKSIITDGPSTYIYPSHSPHTNETIGVLLASYTWSDESLLFLGASDEELK 420
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
362 PWRREHIEGHSNTDRPSRMIFYP-----PPREGALLASYTWSDAAGLRSREAL 416
Oy : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
421 ELALRDLAKIHG---EQWDKCTGVIVKWSADPYSLGAFALFTPYQHLEYAQLFSSE- 476
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
417 RLALDDVAALHGPVVRQLWDG-TGV-VKRWAEQHSQGFVVQPP-----ALWQTEK 466
Oy : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
477 -----GRVHFACEHTAFPHAWIETSMKSAIRAATNIN 508
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
467 DDWTPYGRIFYAGEHTAYPHGWVETAVKSAALRAAIKIN 505
```

RESULT 12

```
US-10-123-904-476
; Sequence 476, Application US/10123904
; Publication No. US20030022328A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C54
; CURRENT APPLICATION NUMBER: US/10/123,904
; CURRENT FILING DATE: 2002-04-16
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 476
; LENGTH: 567
; TYPE: PRT
; ORGANISM: Homo Sapien
```


GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 4, 2005, 13:48:15 ; Search time 43 Seconds
(without alignments)
1172.502 Million cell updates/sec

Title: US-10-645-094-1
Perfect score: 2703
Sequence: 1 MNLHVVKWKLVSIVLITLY.....TNINKVANEESTIHTKDEL 524

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	1059.5	39.2	516	2 JE0266	L-amino-acid oxida
2	1055.5	39.0	516	2 JC8015	L-amino-acid oxida
3	737.5	27.3	446	2 E69899	L-amino acid oxida
4	641	23.7	701	2 JC8062	L-glutamate oxidas
5	412	15.2	526	2 A75581	flavin monoamine o
6	392	14.5	426	2 A12498	L-amino acid oxida
7	392	14.5	695	2 A38114	L-amino-acid oxida
8	383.5	14.2	541	2 A87595	amine oxidase, fla
9	353.5	13.1	534	2 G87384	amine oxidase, fla
10	307	11.4	496	2 H83592	hypothetical prote
11	302	11.2	557	2 A25493	tryptophan 2-monoo
12	288	10.7	520	2 JH0817	amine oxidase (fla
13	287.5	10.6	723	1 S30105	tryptophan 2-monoo
14	285.5	10.6	500	2 T03387	polyamine oxidase
15	283	10.5	527	2 A36175	amine oxidase (fla
16	283	10.5	556	1 A53376	tryptophan 2-monoo
17	271	10.0	520	2 A31870	amine oxidase (fla
18	270.5	10.0	526	2 J0528	amine oxidase (fla
19	269	10.0	471	2 S78290	hypothetical prote
20	267.5	9.9	1265	2 F71429	hypothetical prote
21	265.5	9.8	755	2 A13228	tryptophan 2-monoo
22	259	9.6	755	1 DAAGWT	tryptophan 2-monoo
23	256	9.5	499	2 I51346	monoamine oxidase
24	252.5	9.3	527	2 S03974	amine oxidase (fla
25	251	9.3	755	1 Q0AG4T	tryptophan 2-monoo
26	248	9.2	803	2 T24685	hypothetical prote
27	244.5	9.0	448	2 H70947	hypothetical prote
28	242.5	9.0	478	2 A47693	putrescine oxidase
29	242.5	9.0	516	2 D96682	protein F1e22.18 [

30	240.5	8.9	531	2 S28260	achacin precursor
31	231.5	8.6	483	2 T21327	hypothetical prote
32	231.5	8.6	749	2 I39708	tryptophan 2-monoo
33	225.5	8.3	488	2 T47787	hypothetical prote
34	224.5	8.3	533	2 T09935	hypothetical prote
35	220.5	8.2	508	2 S54021	FMSI protein - yea
36	216	8.0	489	2 A47259	corticosteroid-bin
37	209.5	7.8	770	2 T26783	hypothetical prote
38	205	7.6	490	2 A84861	probable amine oxi
39	198.5	7.3	527	2 T33175	hypothetical prote
40	198.5	7.3	1000	2 T39423	hypothetical prote
41	186	6.9	495	2 S5273	amine oxidase (fla
42	186	6.9	536	2 T24218	hypothetical prote
43	184	6.8	566	2 F71403	hypothetical prote
44	184	6.8	570	2 A39597	phytoene dehydroge
45	183.5	6.8	474	2 S16250	phytoene dehydroge

ALIGNMENTS

RESULT 1

JE0266
L-amino-acid oxidase (EC 1.4.3.2) - eastern diamondback rattlesnake
N:Alternate names: LAAO; ophio-amino-acid oxidase
C:Species: Crotalus adamanteus (eastern diamondback rattlesnake)
C:Date: 05-Feb-1999 #sequence_revision 05-Feb-1999 #text_change 09-Jul-2004
C:Accession: JE0266
R:Arabekas, A.A.; Massey, V. . .
R:Biochem. Biophys. Res. Commun. 248, 476-478, 1998
A:Title: Primary structure of the snake venom L-amino acid oxidase shows high homology .
A:Reference number: JE0266; MUID:98369573; PMID:9703950
A:Accession: JE0266
A:Molecule type: mRNA
A:Residues: 1-516 <RAI>
A:Cross-references: UNIPROT:O93364; GB:AF071564; NID:g3426323; PIDN:AAC32267.1; PID:g3426323
C:Keywords: oxidoreductase

Query Match 39.2%; Score 1059.5; DB 2; Length 516;
Best Local Similarity 44.0%; Pred. No. 1.1e-60;
Matches 218; Conservative 94; Mismatches 171; Indels 13; Gaps 7;

QY	33	LADLCEDKDYDTLLQTLNLGLPHINTSHHVVIVGAGMAGLTAAKLQDAGHTVTILEAND 92	
DB	25	LEECFRETDEEFLIAKNGLTATSNPKRVIVGAGMAGLSAAVYLAGHQVTVLEASE 84	
QY	93	RVGGRVETRYNEKEGWYAEMGAMRIPSSHRIVQWFKVLGVEMNEFVMTDDTTFVLNGV 152	
DB	85	RVGGRVETRYR--KKDWYANLGPMLPTKHRIVREYIKKFDLKLNEFSQENENAWYFIKI 142	
QY	153	RERTVYQENPDVLKYNVSESEKGISADLLDRALOKYKEEVEANGCKAALEKYDRYSVK 212	
DB	143	RKRREVKNPGLLEYPVKPSEEGSAAQLYVESLRKVVEELRSTNCKYILDKYDTYSTK 202	
QY	213	EYLKEGSLPGAVRMIGDLLNEQSLMTALSEMIYDQADVNDSTVYTHEVTGSDLLPEA 272	
DB	203	EYLLKEGSLPGAVDMIGDLLNEDSGYVVSPIESLKHDDIFGYEKRFDEIVGGMQLPTS 262	
QY	273	FLSVL--DVPILLNSKVHRIQSDKGVIVSYQT--GNESLMDLSADIVLVTTTAKAALFI 329	
DB	263	MVEAIKEKVQVHFARVETIQNDREATVTYQTSANEMS--SVTADYVIVCTTSRAARI 320	
QY	330	DFDPLSLSKWEALRSVHSDSTKILLTFROKFWEDDGIKGGKSTIDGPSRVIVYPSHSF 389	
DB	331	KFPEPLPKKAHAALRSVHSGTKIFLTCTKFWEDDGIHGGKSTIDGPSRVIVYPSHSF 380	
QY	390	HTNETIVGLASYTWSDSESLFLGASDEBELKALRLAKIH--GEQVWDKCTGVIVKK 446	
DB	381	TSG--VGVIIA-YGIGDDANFFQALDFKDCADIVINDLSLHELKEDIQTFCHFSMIQR 437	
QY	447	WSADPYSLGAFALFTPYQHLEYAQBELFSSEGRVHFAGEHTAPPHAWITSMKSAIRAAVN 506	
DB	438	WSLDKYAMGGITTTFTPYQHFSEALTAPFKRIYFAGEYTAQFHGWIDSTIKSLGTAARD 497	

QY 507 INKVAEESTIEHTKD 522
Db 498 VNRAENPSGIHLSD 513

RESULT 2
JC8015
L-amino-acid oxidase (EC 1.4.3.2) precursor, TSV-LAO - Chinese green tree viper
N:Alternate names: ophio-amino-acid oxidase
C:Species: Trimeresurus stejnegeri (Chinese green tree viper)
C:Date: 04-Apr-2004 #sequence_revision 04-Apr-2004 #text_change 04-Apr-2004
C:Accession: JC8015
R:Zhang, Y.J.; Wang, J.H.; Lee, W.H.; Wang, Q.; Liu, H.; Zheng, Y.T.; Zhang, Y.
Biochem. Biophys. Res. Commun. 309, 598-604, 2003
A:Title: Molecular characterization of Trimeresurus stejnegeri venom L-amino-acid oxidase
A:Reference number: JC8015, PMID: 12963032
A:Accession: JC8015
A:Molecule type: mRNA
A:Residues: 1-516 <ZHA>
A:Cross-references: GB:AY277739
A:Experimental source: Venom
C:Comment: This enzyme is a flavo-enzyme which catalyzes the stereospecific oxidative deperoxidase (H2O2). TSV-LAO enzyme from venom is a homodimeric, FAD-binding glycoprotein with
C:Genetics:
A:Gene: tsv-lao
C:Keywords: antiviral activity; glycoprotein; L-amino-acid oxidase; snake venom

Query Match 39.0%; Score 1055.5; DB 2; Length 516;
Best Local Similarity 42.8%; Pred. No. 2.1e-60;
Matches 212; Conservative 104; Mismatches 170; Indels 9; Gaps 6;

QY 33 LADCLELDKYDTLLQTLONGPLHINTSHHVIVGVAGMAGLTAAKLQDAGHTVTILEAND 92
Db 25 LSECFTEDTYEFLIARNGLATSNPKHVIVGVAGMGLSAAVLAGAGHEVTVLEASE 84

QY 93 RVGGRVETVRNKEGMYAEMGAMRIPSSHRIVQWFKLVGMENFVMTDDNTFYLVNGV 152
Db 85 RAGGRVTRVNDDEGMYANLGPMLRPEKHRIVREYIRKPNLQNEFSGENDNAWHFVKNI 144

QY 153 RERTVYQENPDVLKYNVSEKGISADLLDRALQKVEEYANGCKAALEKYDRYSVK 212
Db 145 RTVGEVKADPGVLKYPVKPSBEGSAEQLYBESLRKKEKELKRNCSYILNKYDTYSTK 204

QY 213 EYLKEGGLSPGAVRMIGDLLNEQSLMYTALSE-MIYQADVNDVSVTVHEVTGGSDLLPE 271
Db 205 EYLKEGNLSPGAVDMIGDLMNEDAGYVVSFTIESMKHDDIFAYEK-RFDEIVDGMCKLPT 263

QY 272 AFLSLVDVPIILNSVKVHIQSDKGVIVSYQNGNESSLMDLSADIVLVTTTAKAALFIDF 331
Db 264 SMYRAIEEKVHFNAQVIKIQNAEETVTYHT-PEKDTSFVTADYVIVCTTSRAARRIKF 322

QY 332 DPPLSISKMEALRSVHYDSSTKILLTFRDKEWDDGIRGKSIDTGPSSRYIYPSSHSPHT 391
Db 323 EPPLPKKAHALRSVHYRSGTKIFLCTKRFDEGIHGKSTTDLPSRFYIYPNHNFTS 382

QY 392 NETIGVLLASYTWSDESLLFLGASDEELKELALRLAKIH---GQVWDKCTGVTVKWS 448
Db 383 G--VGVIITA-YGIGDANFFQALDKDCGDIVINDLSLIHQLPREIQTFCYPSMIQWS 439

QY 449 ADPSYLGAFALPTPYOHLEYAQELFSSRGRVHFAGEHTAFPHAWTETSMKSAIRAATNIN 508
Db 440 LDKYAMGGITTTPTPYQFQHFSEALTSHVDRIVYFAGEYTAHAHWIDSSIKSLGTAARDVN 499

QY 509 KVANEESTIEHTKDE 523
Db 500 RASENPSGIHLSDND 514

RESULT 3
E69899
L-amino acid oxidase homolog yobN - Bacillus subtilis
C:Species: Bacillus subtilis

C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C:Accession: E69899
R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azavedo, V.; Berter
C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Cho
A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler
iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.P.
Koether, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,
A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel
Y. M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle,
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon,
A:Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seror
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpatra, P.; Tognoni, A.; Tosato, V.; Uchiyama,
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yanane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.
A:Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A:Reference number: A69580; MUID:98044033; PMID:9384377
A:Accession: E69899
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-446 <KUN>
A:Cross-references: UNIPROT:O34363; GB:Z99114; GB:AL009126; NID:g2634230; PIDN:CAB13794.
A:Experimental source: strain 168
C:Genetics:
A:Gene: yobN

Query Match 27.3%; Score 737.5; DB 2; Length 446;
Best Local Similarity 36.4%; Pred. No. 5.3e-40;
Matches 163; Conservative 89; Mismatches 187; Indels 9; Gaps 5;

QY 69 MAGTAAKLQDAGHTVTILEANDRVGRVETRYNE-KEGWYAEMGAMRIPSSHRIVQWF 127
Db 1 MSGLVSASLLKNAGHRTVILEASGRAGRVCTLRASPSDDLIFNAGPMRIPNHSLTLEY 60

QY 128 VKKLGVENPEFMTDDNTFYLVNGVRERTYVQENPDVLKYNVSESEKGISADLLDRAL 187
Db 61 IKKFKLPTNVFINRTPMDIIVANGIKTRLQVFERAPGLIRYPVAPNEQGTSEELMLSL 120

QY 188 QKVKEEVEAN--CCKAALEKYDRYSVKEVYKESGGISPGAVRMIGDLMNQSLMYTALS 244
Db 121 QPILNFINQNPARNRIRIVEBOYKNHSLSSFLNTY--FSYGAIDMIGVLLDMEAYMGSLV 178

QY 245 EMIYDQADVNDVTVYHEVTGGSDLLPEAFLSVLDVPIILLNSKVHQRISQDKGVTVSVYQTG 304
Db 179 EVLRESIFFSPAFHYEITGGMDLLPHAFLPOLKTNILYHQKMMKMGQENRVTIHCHQ 238

QY 305 NESSLMDLSADIVLVTTTAKAALFIDFPPLSIS--KMEALRSVHYDSSTKILLTFRDKF 362
Db 239 QTAEFTSTADLAIVTIPFSTLRFVKVEPVHSPSYKRRRAIRELNYISATKIGIEFKSRF 298

QY 363 WEDDGIRGKSITDGPSSRYIYPSSHFTNETIGVLLASYTWSDESLLFLGASDEELKEL 422
Db 299 WEKAGQHGKSIDTLPPIRFYSYPSRNTGANGH-AVILASYTWAEALIWDSLSSEGERIQY 357

QY 423 ALRLAKIHGEQVWDKCTGVIVKWSADPYSLGAFALPTPYOHLEYAQELFSSRGRVHFA 482
Db 358 TLLNLSIYGDIVWSEFVSGTSFSWSQYPSYAGSGTAFEPQOELELIPYIPVPGRVHFA 417

QY 483 GEHTAFPHAWTETSMKSAIRAATNINKV 510
Db 418 GEHASLTHAWQGAIESGIRVAVEVNR 445

RESULT 4
JC8062
L-glutamate oxidase (EC 1.4.3.11) precursor - Streptomyces sp.
C:Species: Streptomyces sp.
C:Date: 09-May-2004 #sequence_revision 09-May-2004 #text_change 09-May-2004
C:Accession: JC8062
R:Arima, J.; Tamura, T.; Kusakabe, H.; Ashiuchi, M.; Yagi, T.; Tanaka, H., and Inagaki,
J. Biochem. 134, 805-812, 2003
A:Title: Recombinant expression, biochemical characterization and stabilization through

A:Reference number: JC8062; PMID: 14769868
A:Accession: JC8062
A:Molecule type: DNA
A:Residues: 1-701 <ARI>
A:CROSS-references: DDBJ:AB085623
A:Experimental source: (Strain X-119-6)
C:Comment: This enzyme precursor is a protein of 150K with hexamer structure alpha2-beta2
ns non-covalently bound FAD as a cofactor. It catalyzes the oxidative deamination of an
in quantitative assaying of L-glutamate existing in food and in a fermentation process.
C:Genetics:
A:Gene: Lgox
A:Start codon: GTG
C:Keywords: hexamer structure; L-glutamate oxidase

Query Match		23.7%;	Score 641;	DB 2;	Length 701;
Best Local Similarity		27.2%;	Pred. No. 1.8e-33;		
Matches 170;		Conservative 95;	Mismatches 195;	Indels 164;	Gaps 14;
QY	49	LONGPLPHINTSHHVIVGAGMAGLTAALKLQDAGHTVTILEAN-DRVGRVETYNKEK--	105		
DB	48	INDGNLPPGPPKRLILVAGIAGLVAGDILLTRAGHDVTILEANARVGGRIKTFHAKKGE	107		
QY	106	-----EGYVAGMAMRIPSSHRIVQWFKVLGVEMNEFVMTDDN-----TFY	147		
DB	108	PSFADPAQYAGAMRLFSFHLTLALIDKLKRLRFNFVDIDPOTGNQDAPVPVPY	167		
QY	148	-----LVNGV-----RERTYVQENPDVLK-----YNVSESEK	176		
DB	168	KSFQDKGTWNGAPSPFEPKPKRHNHTWIRTNREQVRRQAQYATDPSSINEGFHLTGCTR	227		
QY	177	ISADLLDRALQKVEEVAN-----GCKAALEKYDYSVKEYLKEEGG	220		
DB	228	LTVDVMVNAQLEPFVDYSVKQDDGTRVKNPKFEMLAGWADVDFDGYSMGRFLREYAE	287		
QY	221	LSPGAVRMIGDLNLSQSLMYTALSEMIYQADVNSVTYHETGSDLLPEAFSLVLDVP	280		
DB	288	FDEAVEAIGTIENNTSRHLAFTHSFLGRSDIDPRATYWEIEGGRMLPETLAKDLRDQ	347		
QY	281	ILLNSKVHRIOSDK-----QVIVSYQTGNE-----SSLMDLSADIVLVTTTA	323		
DB	348	IVMGQRMVLEYYDFCRDGHGELTCGCPGPAVAIQVPEGEFYAATQTWGLAIVTIPF	407		
QY	324	KAALFIDPDPPLSISKMEALRSVHVDSTKILLTTRDKFW-----	363		
DB	408	SSLRFVKVTPPFSYKRRRAVIETHYDQATKVLLEFSRRWTEADWKRELDIAIAPGLYD	467		
QY	364	-----EDD-----GIR---	369		
DB	469	YYQQNGEDDAEALALPQSVRNLPGLLGAHPSVDESIRIGEQVEYRNSELRGVVRPAT	527		
QY	370	---GGKSITDGPSTYIYPSHSFHTNETIGVLLASVTWSDLSLLFLGASDEELKELALRD	426		
DB	528	NAYGGSTTDNPNRMYPYSHVPVGTQG-GVVLAYSNSDDAARWDSFDDAERYGVALEN	586		
QY	427	LAKINGEQWMDCTGV-IVKWSADPYSIGAFALFTPYQHLEYAQELFSSEGRVHFAGEH	485		
DB	587	LQSVHGRRIEVTGAGTQSLRDPYACCEAAVYTPHQMTAFHLDDVVRPEGPVYFAGEH	646		
QY	486	TAPPHAWIETSMKSAIRAATNINK	509		
DB	647	VSLKHAWIEGAVETAVRAAIYNE	670		

RESULT 5
A:Reference number: AB1807; PMID: 21595285; PMID: 11759840
A:Accession: A12498
A:Molecule type: DNA
A:Residues: 1-426 <KUR>
A:CROSS-references: UNIPROT:Q8YKX9; GB:BA0000020; PIDN:BAB78253.1; PID:gl7135707; GSPDB:1
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999

A:Title: Genome sequence of the radioreistant bacterium Deinococcus radiodurans R1.
A:Reference number: A75250; PMID:20036896; PMID:10567266
A:Accession: A75581
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-526 <WHI>
A:CROSS-references: UNIPROT:Q9RYN6; GB:AE001863; GB:AE001825; NID:g6460670; PIDN:AAF124
A:Experimental source: strain R1
C:Genetics:
A:Gene: DRA0274
A:Map position: 2

Query Match		15.2%;	Score 412;	DB 2;	Length 526;
Best Local Similarity		27.5%;	Pred. No. 6.7e-19;		
Matches 140;		Conservative 86;	Mismatches 194;	Indels 90;	Gaps 18;
QY	62	VVVGAGMAGLTAALKLQDAGHTVTILEANDRVGRVETYNKEK-----	106		
DB	51	VLLGGGLAGASAYEMQKAGYDVQVLLFENGGRAGRCWTIRGGDEYTELGGFKQTCFDR	110		
QY	107	GWYAEAGMAMRIPSSHRIVQWFKVLGVEMNEFVMTDDNTFYLVNG-----VRE--R	155		
DB	111	GLYINPGWPWRIPCHHHAYLVHVARBEVGKLEPFIMENMNAYIHREGKNGQOPTVRVQAEAR	170		
QY	156	TYVQENPDVLKYNVSES--EKGISADLLDRALQKVEEVANGCKAALEKYDXY----	209		
DB	171	TDMQGHVAELLNKAASQGNLDTGLTTED-----KEKLEALHEWG---FLNKDGRYVKSL	222		
QY	210	---SVKEYLKEEGG-LSPGA-VRMIG-DLLNEQSILMYTALSEMIYQADVNSVTYH---	260		
DB	223	ETSTFRGVDROPGARLEFGTSPQPLGLDTLLERRLW-----SDLNQGMVYEFRS	271		
QY	261	---EVTGSDLLPEAFSLVDLPVILLNSKVHRIOSDKGVIIVSYQTGNESSLMDLSADIV	317		
DB	272	TMFEPVGMGAMARAFESRVRGFIKYRARVTEIKDQTKVTATY-VDADGTTKTASGDYC	330		
QY	318	LVTTTAKAALFIDPDPPLSISKM-----BALRSVHYDSSTKILLTTRDKFWE-D	365		
DB	331	ICTI-----PLSILSQIKLTGVDKDLAEAIKKVPYASSFKAGVOYKRRFWEQD	378		
QY	366	DGIRGKSITDGPSTYIYPSHSFHTNETIGVLLASVTWSDLSLLFLGASDEELKELALR	425		
DB	379	DDIYGGISYTDLPNQLISYPNNYFSTGK-GVVLGAYMFGTDVAVVNSGMSPEERLUKKVVE	437		
QY	426	DLAKIHGEQWMDCTGVIVKWSADPYSIGAFALFTPYQHLEYAQELFSSEGRVHFAGEH	485		
DB	438	YNAQLHPAAAKEFDNGVTV-GMHRVPWTLCGYGLYNADTRERYYPYTLCAHGRMLAGEH	496		
QY	486	TAPPHAWIETSMKSAIRAATNINKVNEES	515		
DB	497	TSYVNWQEGALLAATTAQVQEMHKFASQA	526		

RESULT 6
A12498
L-amino acid oxidase [imported] - Nostoc sp. (strain PCC 7120) plasmid pCC7120alpha
C:Species: Nostoc sp. PCC 7120
A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C:Accession: A12498
R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi,
Nakazaki, N.; Shimo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, E.
DNA Res. 8, 205-213, 2001
A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
A:Reference number: AB1807; PMID:21595285; PMID:11759840
A:Accession: A12498
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-426 <KUR>
A:CROSS-references: UNIPROT:Q8YKX9; GB:BA0000020; PIDN:BAB78253.1; PID:gl7135707; GSPDB:1
A:Experimental source: strain PCC 7120
C:Genetics:
A:Gene: alr7169

A:Genome: plasmid

[illegible][illegible]

Query Match	14.2%	Score 383.5	DB 2	Length 541	
Best Local Similarity	26.7%	Pred. No. 4.8e-17			
Matches 131	Conservative	92	Mismatches 209	Indels 59	Gaps 15
Qy	62	VTVVGAGMAGLTAAKLLQDAGHTVTILEANDRVGGRVETVR-----NEKEG--	108		
Db	66	VIVLGAGLGLAAAFELRAKAGYKVQILFQNRPGCRNWSLRGGDSYTELGGATQKVGYAA	125		
Qy	109	--YAEGMAMRIPSSHRIVQWFKVLGVEMNEFVMTDDNTFTVLVNGVRERTTVVQENPDVL	166		
Db	126	GNVFNEPGWRIPHHHRTLLHYCKQFGVAALEPFTQFNH-----SGWIHSSQAFGKGP--	177		
Qy	167	KYNVSESE-----KGISADLLDLRALQKVKEE--VEANGCKAALEKVDRY-----	209		
Db	178	RFNAAADPFGNTAEALLAKSVNAKALDDAVTLEDRERLLLEALKGWGMLDKDYRYAASLR	237		
Qy	210	-SVKEYLKEGGSLSPGA-----VRMTGDLNLEQOSLMYTALSEMIYQOADVNDVSVTYHEV	262		
Db	238	SSRHGFKRPGGGVGDGAPIESDLYLSHVDLPQ--VMTSGMFGFMNHM-----QTTMFQP	291		
Qy	263	TGGSDLLPEAFSLVDVPIILNKSVKHROSDDKGVIVSYOTGNESSLMDLSADIVLVTTT	322		

Query Match	14.5%	Score 392;	DB 2;	Length 695;
Best Local Similarity	27.0%;	Pred. No. 2e-17;		
Matches 148;	Conservative 90;	Mismatches 195;	Indels 116;	Gaps 26
Qy	37	LEDKDYDTLLQTLNDGLPHINTSHVVIVGAGMAGLTAALKLQDAGHT-VTILEANDRVG	95	
	:	: :	: :	: :
	:	: :	: :	: :
Db	160	LEDKE-----ISTVD---VEKAKSKNIAIVGAGMSGLMTYLCLTQAGTNTVSIIEGGRNLG	212	
	:	: :	: :	: :
	:	: :	: :	: :
Qy	96	GRVET-----YRNEKEGHWYEMGAMRIP-----SSHRIV-----	124	
	:	: :	: :	: :
	:	: :	: :	: :
Db	213	GRVHTYLSGGPPDYS-----YQEMGPMRPFNITLGNVTYNSDHLQVFLQAEWNLSL	266	
	:	: :	: :	: :
	:	: :	: :	: :
Qy	125	QWPFVKLLGVEMNEFVMTDDNTDFYLVNGVRERTYVYVQENPDV-LKYNVSESEKGISADDLL	183	
	:	: :	: :	: :
	:	: :	: :	: :

Db 292 VCGMDMIGKAFQVGEGLITYNAKVSIAQDDKGVVVYADTVTGKVTAKGD--WCVCT 349
Qy 323 AKAAALFIDPDPPLSISKMEALRSVHYDSSTKILLTPDKFW-EDDGIRGGSITDGPSTY 381
Db 350 IPLGILGQMDLAVTDEMMAIKAVPVSQGVKGLMNRFRWEDDDIYGGHFTDQIEGL 409
Qy 382 IYPSHSHFTNETIGVLLASYTMSDESLFLFGASDEELKELALDLAKIHGQVMDKC-T 440
Db 410 ISVPNNLF-QDGPVLLGAFARDLCAFRLAGWTPEORIEVALAQGSVHPKSYRKEPT 468
Qy 441 GVIVKWSADPVSGLAFALFTPYQHLEYAQELFSSEGRVHFAGEHTAFPHAMTSMKA 500
Db 469 GASV-AWSVPVTLGCGARWNEETRKHQYQTLVAMDRIRVLAGEHASYVGCWMEGALLSS 527
Qy 501 IRAATNINKVA 511
Db 528 LDAITRLHKRA 538

RESULT 9
G87384
amine oxidase, flavin-containing [imported] - Caulobacter crescentus
C:Species: Caulobacter crescentus
C:Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C:Accession: G87384
R:Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
n, J.; Emolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A:Title: Complete Genome Sequence of Caulobacter crescentus.
A:Reference number: A87249; MUID:21173698; PMID:11259647
A:Accession: G87384
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-534 <STO>
A:Cross-references: UNIPROT:Q9A9A3; GB:AE005673; NID:G13422395; PIDN:AAK23075.1; GSPDB:G
C:Genetics:
A:Gene: CC1091

Query Match 13.1%; Score 353.5; DB 2; Length 534;
Best Local Similarity 27.8%; Pred. No. 46-15;
Matches 141; Conservative 64; Mismatches 226; Indels 77; Gaps 17;

Qy 48 TLDNGLPHINTSHHVIVGAGMAGLTAAKLLQDAGHTVTILEANDRVGGRVETRYNE--- 104
Db 51 TLTGAK--NTK--VILGAGLAGTAAAYEMSKAGYQVILPARYAGRCQTARKGFKH 106
Qy 105 -----KEGYAEMGAMRIPSSHRIYQVFKVLGVEMNBFVMTDDNTF--YLNG 151
Db 107 TDLGNTQVCEPDDGHYINHGAWRIPYHHRSTLHYTKSFGVLLESFVNDNDASYVPEKG 166
Qy 152 VRERYVQENPDVLKYNVSESEKISADLLDRALQKVEVEANGCKAALEKYDRYSV 211
Db 167 -----KGP-----LNGKPVKGEIAADVRYTAELVAKAASAGALDAPLSGVDRERF 213
Qy 212 KEYLKEEGLS-----PGAVRMIG-----DLLNEQSLMYTAL 243
Db 214 VAYLVNEGRLSKDLTYKTEGRGFSVHPGAGNPGPKELEPPAFKQVLDNSA--WRVL 271
Qy 244 SEMI-YDQADVNDSTYHVTGSDLLPEAFSLVDLPILNLSKVKHIRQSDKGIVISYQ 302
Db 272 SSVTGYEQ-----QRTMLQPIGMDQIAKAFKRVAPMIRYSTVVQIKQSPGTGTVSFK 326
Qy 303 TGNESLMDLSADIVLVTTAKAALFIDPDPPLSISKMEALRSVHYDSSTKILLTPDKF 362
Db 327 -GPDGKLGVTADYCVCTIPLSVLQIDLD--ASAPFKAAMEGVAYAPVNIKGLQMKSRF 383
Qy 363 WED-DGIRGGSITD-GPSRYIYPSHSHFTNETIGVLLASYTMSDESLFLFGASDEELK 420
Db 384 WEDRHHIYGGHIYTLAGIGSISLPSGWQAQK--GVLLGYAFGEAAISAKSPADRA 441
Qy 421 ELALRDLAKIHGEQVWDKCTGVIVKWSADPVSGLGAFALFTPYQHLEYAQELFSSEGRVH 480

Db 442 AFAVAGGQKVPPEYA-ENFENAFPSWHLAEHLNLCGWAEGNRKEAYPILCEPDGRLY 500
Qy 481 PAGEHTAFPHAMTSMKSAIRAATNIN 508
Db 501 LAGEHLSYLGGMQAGAISSAQOIAKIH 528

RESULT 10
H83592
hypothetical protein PA0421 [imported] - Pseudomonas aeruginosa (strain PA01)
C:Species: Pseudomonas aeruginosa
C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C:Accession: H83592
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warriner, P.; Hickey, M.J.; B.
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic path
A:Reference number: A82950; MUID:20437337; PMID:10984043
A:Accession: H83592
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-496 <STO>
A:Cross-references: UNIPROT:Q9I692; GB:AE004479; GB:AE004091; NID:G9946272; PIDN:AAG0381
A:Experimental source: strain PA01
C:Genetics:
A:Gene: PA0421

Query Match 11.4%; Score 307; DB 2; Length 496;
Best Local Similarity 27.0%; Pred. No. 3-6e-12;
Matches 129; Conservative 83; Mismatches 200; Indels 66; Gaps 20;

Qy 63 VIVGAGMAGLTAAKLLQDAGHTVTILEANDRVGGRVETRYNEKEGYAEMGAMRI-PSSH 121
Db 31 IWVGAGLAGLSAAAYELQDQGVTVLEARPQVGRSGLATSE---W---VGQKQVQPTLN 84
Qy 122 RIVQWFKVLGVEMNEFVMTDDNTFYLNVGRERTYVYVQENPDVLKYNVSE---SEKGS 178
Db 85 AYLDTF-KLKPVPAPDFVTRPS---YLIDG-----LYYSSDDLALQPNVA 126
Qy 179 AD-----DLLDRALQKVEVEANGCKAALEKYDRYSVKYKLEGGSLSPGAVRMIG 230
Db 127 ADLKRFEFTLDDLSGISDPLNPASSN---TLFALDQMAARWL-DKLNLSPTARLLVN 181
Qy 231 DLLNEQ-----SLMYTALSEMIYDQADVNDSTYHVTGSDLLPEAFSLVDLPILL 283
Db 182 QRIRSRVDEPSRSLSLYLAQQRAYRGVDDRD-LRAARLPQGSQVLAFAFVKQIKT-IKT 239
Qy 284 NSKVKHIRQSDKGIVTSYOTGNESLMDLSADIVLVTTAKAALFIDPDPPLSISKMEAL 343
Db 240 KSKVSSIVQAKGVAV--KAGSET-----YKADYVVVLAIVPLKALGOIQMTPSLSGTQMSAL 293
Qy 344 RSVHYDSSTKILLTPDKFWEDDGIRGGSITDGPSTYIYV-PSHSHFTNETIGVLLASY 402
Db 294 KGTNYGWRDQILLKFKRPVWDDKSRLSGEIPIFSDQGLGMIWVEPALKGCANVLINLS---- 349
Qy 403 TWSDESLFLFGASDEELKELALDLAKIHGQVWDKCTGVIVKWSADPVSGLGAFALFTP 462
Db 350 --GDNARVLQAFGRQMVQDVLIRMKFY-PKMRGAFAGYIIRRYASDPGTGGSYLAYGP 406
Qy 463 YQHLEYAQELFSSEGRVHFAGEHT-APPHAMTSMKSAIRAATNINKV-ANEESTIE 518
Db 407 QQVTRFRWIRWEQPLSRVAFAGEHTDALYPGTIEGALRSKGAASQVRDLAYAGTKTPVIE 464

RESULT 11
A25493
tryptophan 2-monooxygenase (EC 1.13.12.3) - Pseudomonas syringae pv. savastanoi
C:Species: Pseudomonas syringae pv. savastanoi
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C:Accession: A25493
R:Yamada, T.; Palm, C.J.; Brooks, B.; Kousuge, T.

Proc. Natl. Acad. Sci. U.S.A. 82, 6522-6526, 1985

A;Title: Nucleotide sequences of the Pseudomonas savastanoi indoleacetic acid genes show
A;Reference number: A94062
A;Accession: A25493
A:Molecule type: DNA
A;Residues: 1-557 <YAM>
A;Cross-references: UNIPROT:P06617
C;Genetics:
A;Gene: iamM
C;Superfamily: Pseudomonas tryptophan 2-monoxygenase
C;Keywords: monoxygenase; oxidoreductase

Query Match 11.2%; Score 302; DB 1; Length 557;
Best Local Similarity 24.8%; Pred.No.9e-12;
Matches 129; Conservative 83; Mismatches 202; Indels 106; Gaps 18;

QY 62 VVIVGAGMAGLTAALKLLDQAG-HTVTILAEANDRVGRV--ETYRNEKEGWYAEMGMRRP 118
 |||||:::||
Db 41 VALVGAGISGLVANATELLRAGVKDVVLYESDRIGRGWMSQVFDTQRPPIAIEMGMARFP 100

QY 119 SSHRIYQWFVKKLGVMENFVV---MTDDNTFYLVNGVRERTVVQDENPVLYKNVSESE 174
 ::|||:::
Db 101 PSATGLFHYLKFGISTSTTFDPDGVVDTELHV--RKRYHHPACKPKPELFPRVVEGGQ 158

QY 175 KGISADDDLRLALOKVKEEVAENGCAALEKY----- 206
 :||||:
Db 159 SULLSEGYLEGGSLVAPLDITAMLKSRLFEAAIAQQWLNVFRDCSFYNAlVCFTGRH 218

QY 207 ----DRYSKVKEYKEEGGLSPGARVMIGDLNSEQSIWTALSEMIYD--QAENVDSVTYH 260
 ||||:|::|
Db 219 PGGDWARPEDEFELFGSLGIS----GGFLVPFOAGFTEILLRMVINGYQSD----- 266

QY 261 EVTGSGDLLPEAFPSV-----LDVPILL---SKVGHIRQSODKGVIYSQTGNES 308
 |::|:
Db 267 -----QLLPDGISSLAARLABQSPDKAIRDVCFSRVGRISRAREAKIIIQTEAGEQRV 321

QY 309 LMDLSNDIYLVTTTTAKAALI-----DFDPLSISKWEALRSVHYDSSTKKILLTPFDKPWE 364
 ||||:|::|
Db 322 F-----DRVIVTSNRAMQMHIChLTDESFSLRDVARAVRETHLTGSCKLFIILTETKW- 375

QY 365 DDGI RGKGSKIT---DGPGRYIYPGSHSFHTNETICIGLLASYTWSDESLFLFCASDELK- 420
 |||||:
Db 376 ---IKNKLP TTI Q SD LG RVGYCLDYQ D DEPGHGVLVS YTWEDDAQKLAMP DK KTR C 432

QY 421 ELALRD LA KHGEQV-----WDKCTGV IV VKNS AD PY SL GA FA LF PP YO HLE VA O E L F 473
 ::|||:
Db 433 QVLVDDLA AI HP TP AS Y LL PV DG DY ER VL HH DM LT DP HS AG AF KL NV PG ED V -YS QR LP 491

QY 474 -----SS EG R VH FA GE HT AP PH AM I ET SM KS AIR AA 504

492 FQP MT AN SP NK DT GL Y L AG CS CG SC FAG GW IE GA VO TAL NS A 531

RESULT 12
JH0817
amine oxidase (flavin-containing) [EC 1.4.3.4] B - human
N:Alternate names: monamine oxidase B
S:Species: Homo sapiens (man)
C:Accession: JH0817; JH0818; B36175; 162455; S66431
D:Date: 30-Sep-1993 #sequence revision 20-Aug-1994 #text_change 09-Jul-2004
A:Accession: JH0817; JH0818; B36175; 162455; S66431
J. Neurochem. 61, 187-190, 1993
T:Title: The deduced amino acid sequences of human platelet and frontal cortex monoamine
R:Reference number: JH0817; MUID:93294582; PMID:8515265
A:Accession: JH0817
M:Molecule type: mRNA
R:Residues: 1-520 <CH1>
C:Cross-references: UNIPROT:P27338; GB:S62734; NID:g398414; PIDN:AAB27229.1; PID:g398415
E:Experimental source: platelet
A:Accession: JH0818
M:Molecule type: mRNA
R:Residues: 1-520 <CH2>
C:Cross-references: GB:S62734; NID:g398414; PIDN:AAB27229.1; PID:g398415

A;Experimental source: cerebral cortex
R;Bach, A.W.J.; Lan, N.C.; Johnson, D.L.; Abell, C.W.; Bembenek, M.E.; Kwan, S.W.; Seebach, Proc. Natl. Acad. Sci. U.S.A. 85, 4934-4938, 1988
A;Title: cDNA cloning of human liver monoamine oxidase A and B: molecular basis of difference
A;Reference number: A36175; MUID:88263063; PMID:3397449
A;Accession: B36175
A;Molecule type: mRNA
A;Residues: 1-520 <BAC>
A;Cross-references: GB:M69135; GB:J03793; NID:g187374; PIDN:AAA59551.1; PID:g187376
A;Experimental source: tissue liver
A;Note: parts of this sequence were determined by protein sequencing
R;Zhu, Q.S.; Grimsby, J.; Chen, K.; Shih, J.C.
J. Neurosci. 12, 4437-4446, 1992
A;Title: Promoter organization and activity of human monoamine oxidase (MAO) A and B genes
A;Reference number: I41054; MUID:93057796; PMID:1432104
A;Accession: I62455
A;Status: preliminary; translated from GB/EMBL/DBD
A;Molecule type: DNA
A;Residues: 1-15 <RES>
A;Cross-references: GB:M89637; NID:g187378; PIDN:AAB46386.1; PID:g553527
A;Experimental source: cell-line 1635
R;Cesura, A.M.; Gortowik, J.; Lahm, H.W.; Lang, G.; Imhof, R.; Malherbe, P.; Roethlisberger, J. Biochem. 236, 996-1002, 1996
A;Title: Investigation on the structure of the active site of monoamine oxidase-B by affinity labeling
A;Reference number: S66431; MUID:96270755; PMID:8665924
A;Accession: S66431
A;Molecule type: Protein
A;Residues: 371-391 <CES>
C;Genetics:
A;Gene: GDB:MAOB
A;Cross-references: GDB:119377; OMIM:309860
A;Map position: Xp11.23-Xp11.23
C;Function:
A;Description: catalyzes the oxidative deamination of many neurotransmitters and dietary
A;Keywords: dimer; FAD; flavoprotein; mitochondrion; oxidoreductase; phosphoprotein
F;6-34/Region: beta-alpha-beta FAD nucleotide-binding fold
F;397/Modified site: S-(Galpha-FAD)-cysteine (Cys) #status predicted

	Query Match	Best Local Similarity	10.7%;	Score 288;	DB 2;	Length 520;
	Matches 131;	Conservative	84;	Mismatches 169;	Indels 140;	Gaps 27;
Qy	62	VIVGAGMAGITAAKLQDAGHTVITLBNDRVGRVETYRNEKEGWAEMGAMRI-PSS 120				
Db	7	VVVGGTSGMAAAKLLHDSGLNVVLEARDRVGGRTVTLRQKVK-YVDLGGSYVGPQ 65				
Qy	121	HRIQVQFVKVLGVE---MNEFVMTDDNTFYLVNGVRETYVVOE-----NDVLKYNVS 171				
Db	66	NRILR-LAKELGLEYTKNEVER-----LIHHVKGSKSYPRGPPPPVWNP--ITY--- 112				
Qy	172	ESEKGISADDLLD-----RALQKVEEVEANG-KAAL-EKYDRVSVKEYLKEEGSLSPG 224				
Db	113	-----LDHNNFRWTDMDGREGTPSDAPWKAPLAEWDNWTMKELL----- 152				
Qy	225	AVRMIGDLLNEQSLMYTALSSEMIYQDQDVDSVT--YHEVT----- 263				
Db	153	-----DKLCWTESAKQL-ATFWNLCVTAETHEVSALWFLWTVKQCGTTRIIS 200				
Qy	264	-----GGSDLLPEAFSLVDVPILNLSKVHQRQSDKGVISVQTGNESSLMDL 312				
Db	201	TTNGGQERKFVGGSGQVSERIMDLLGDRVKLERPVYIDQTRENVLV--ETLNHEM---Y 255				
Qy	313	SADIVLVTTTAKAALFDPPPLSISKWEALRSVHYQSTKILLTFRDKFWDDGIRGK 372				
Db	256	EAKVISAIPPTLGMKIHFNPLPMNOMITRVPGLSVIKCIYVYKEPFWKKDY-CGT 314				
Qy	373	SITDGPSTRIYV-----PSHSFHTNETIGVLLASYSWDSDESLFLGASDEELKEL---- 422				
Db	315	MIIDGEEAPVAYTLDDTKPEGNYAA--IMGFILAHKARKLARL-----TKERLKKLCELY 368				
Qy	423	-----ALRDLAKIHGEQVWDKCTGIVVKWSADPYSIGAFALFTPYQHL-EYAGELFSE 476				
Db	369	AKVLGSLAEALPHYEE-----KNWCEQYSGGCYTYFPFGILLTOYGRVIRQPV 418				

Search completed: October 4, 2005, 14:04:27
Job time : 47 secs